

```

DR EMBL; AF364814; AAK83297.1; -
DR EMBL; AF364815; AAK83298.1; -
DR EMBL; AF364816; AAK83299.1; -
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR PROSITE; PS50017; DEATH DOMAIN; FALSE NEG.
DR PROSITE; PS00652; TNFR_NGFR_1; FALSE NEG.
DR PROSITE; PS00652; TNFR_NGFR_2; FALSE NEG.
DR PROSITE; PS00652; TNFR_NGFR_3; FALSE NEG.
DR Receptor; Developmental protein; Differentiation; Apoptosis;
KW Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 27
FT CHAIN 28 514
FT FT
FT DOMAIN 28 183
FT TRANSMEM 184 204
FT DOMAIN 205 514
FT DOMAIN 403 476
FT REPEAT 31 72
FT REPEAT 74 114
FT REPEAT 116 149
FT REPEAT 139 149
FT DISULFID 32 45
FT DISULFID 48 61
FT DISULFID 51 72
FT DISULFID 75 88
FT DISULFID 94 114
FT DISULFID 117 136
FT DISULFID 139 149
FT CARBOHYD 39 32
FT CARBOHYD 58 58
FT VARIANT 13 13
FT VARIANT 155 155
FT VARIANT 353 353
SQ SEQUENCE 514 AA; 56066 MW; 82C7F0661EECFB48 CRC64;

Query Match 59.7%; Score 37; DB 1; Length 514;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRPQGE 6
Db 51 CRPQGE 56

RESULT 12
YMSO YEAST STANDARD; PRT; 515 AA.
AC Q03264;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical 59.5 kDa protein in Hdf1-MRPL33 intergenic region.
GN YMR285C OR YMR021.11C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX MEDLINE=97311268; PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagsis K., Lye G., Mout R., Odell C., Pearson D., Rajadream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrall B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
XIII."
RL Nature 387:90-93(1997).
CC -1- SIMILARITY: Belongs to the CCR4/NOTURIN family.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z49704; CA89783.1; -
DR PIR; S54592; S54592.
DR GerMOnline; 142960; -
DR SGD; S0004898; YMR285C.
DR GO; GO:0005622; Cintracellular; IDA.
DR GO; GO:0004521; F:endoribonuclease activity; IMP.
DR GO; GO:0006364; P:RNA processing; IMP.
DR InterPro; IPR005135; Exo endo_phos.
DR Pfam; PF03372; Exo endo_phos; 1.
KW Hypothetical protein.
SQ SEQUENCE 515 AA; 59539 MW; 89B30A7D24D6EBC8 CRC64;

Query Match 59.7%; Score 37; DB 1; Length 515;
Best Local Similarity 47.1%; Pred. No. 28;
Matches 8; Conservative 1; Mismatches 2; Indels 6; Gaps 1;

Qy 1 CR-----PGQLTKQG 11
Db 477 CRGFLRPPQNTWKHG 493

RESULT 13
KCH8 MOUSE STANDARD; PRT; 876 AA.
ID KCH8 MOUSE
AC P59111;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Potassium voltage-gated channel subfamily H member 8 (ether-a-go-go-
DE like potassium channel 3) (ELK channel 3) (ELK3) (Fragment).
GN KCH8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Retina;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg K.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg K., Buetow K.H., Buetow K.H., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Shapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium
CC channel. Elicits a slowly activating, outward rectifying current
CC (By similarity). Channel properties may be modulated by cAMP and
CC subunit assembly (By similarity).
CC -1- SUBUNIT: The potassium channel is probably composed of a homo- or
CC heterotetrameric complex of pore-forming alpha subunits that can
CC associate with modulating beta subunits.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is

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CC characterized by a series of positively charged amino acids at  
 CC every third position.  
 CC -1- SIMILARITY: Belongs to the potassium channel family. H (Bag)  
 CC subfamily.  
 CC -1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.  
 CC -----  
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 CC -----  
 DR EMBL: BC029690; AAH29690.1; -  
 DR MGI: 2445160; C13009D008Rik.  
 DR InterPro: IPR000595; CNMP binding.  
 DR InterPro: IPR003967; Erg\_Channel.  
 DR InterPro: IPR005821; Ion\_trans.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR005820; M+channel\_nlg.  
 DR Pfam: PF00027; CNMP\_binding; 1.  
 DR Pfam: PF00520; Ion\_trans; 1.  
 DR PRINTS: PR01470; ERGCHANNEL.  
 DR SMART: SM00100; CNMP; 1.  
 DR PROSITE: PS00888; CNMP\_BINDING\_1; FALSE\_NEG.  
 DR PROSITE: PS00889; CNMP\_BINDING\_2; FALSE\_NEG.  
 DR PROSITE: PS50042; CNMP\_BINDING\_3; 1.  
 DR Transport; Ion transport; Ionic channel; Voltage-gated channel;  
 KW Potassium channel; Potassium; Potassium transport; Transmembrane;  
 KW Glycoprotein; Multigene family.  
 FT NON\_TER 1 1  
 FT TRANSMEM <1 1 SEGMENT S1 (POTENTIAL).  
 FT TRANSMEM 30 50 SEGMENT S2 (POTENTIAL).  
 FT DOMAIN 51 72 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 73 93 SEGMENT S3 (POTENTIAL).  
 FT TRANSMEM 102 122 SEGMENT S4 (POTENTIAL).  
 FT DOMAIN 123 127 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 128 148 SEGMENT S5 (POTENTIAL).  
 FT DOMAIN 194 214 SEGMENT H5 (PORE-FORMING) (POTENTIAL).  
 FT TRANSMEM 223 243 SEGMENT S6 (POTENTIAL).  
 FT DOMAIN 244 276 CYTOPLASMIC (POTENTIAL).  
 FT NP\_BIND 325 442 CNMP.  
 FT DOMAIN 485 496 POLY-GLU.  
 FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 876 AA; 97486 MW; 83F60290F4C3FE0C CRC64;  
 Query Match 59.7%; Score 37; DB 1; Length 876;  
 Best Local Similarity 54.5%; Pred. No. 50;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CRPQBLTXQ 11  
 Db 346 CAPGEVLLRQ 356  
 RESULT 14  
 Z445\_MOUSE  
 ID Z445\_MOUSE STANDARD; PRT; 986 AA.  
 AC Q8R2V3; Q8K216;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Zinc finger protein 445.  
 GN ZNF445.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;

RA Zhou G., Wang J., Zhang Y.;  
 RT "Cloning of mouse zinc finger protein 445.";  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 RN (2)  
 RP SEQUENCE OF 345-986 FROM N.A.  
 RX MEDLINE=22398257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Boudado M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: May be involved in transcriptional regulation.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-  
 CC FINGER PROTEINS.  
 CC -1- SIMILARITY: Contains 1 KRAB domain.  
 CC -1- SIMILARITY: Contains 1 SCAN box domain.  
 CC -1- SIMILARITY: Contains 12 C2H2-type zinc fingers.  
 CC -----  
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 CC -----  
 DR EMBL: AY341877; AAQ24161.1; -  
 DR EMBL: BC027167; AAH27167.1; -  
 DR EMBL: BC034572; AAH34572.1; ALT\_INIT.  
 DR MGI: 2143340; AW610627.  
 DR InterPro: IPR007087; Znf\_C2H2.  
 DR Pfam: PF00096; zf-C2H2; 12.  
 DR SMART: SM00355; Znf\_C2H2; 12.  
 DR PROSITE: PS00805; KRAB; 1.  
 DR PROSITE: PS00804; SCAN\_BOX; 1.  
 DR PROSITE: PS00028; ZINC\_FINGER\_C2H2\_1; 12.  
 DR PROSITE: PS00157; ZINC\_FINGER\_C2H2\_2; 12.  
 DR Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;  
 KW Nuclear protein; Repeat.  
 FT DOMAIN 52 134 SCAN\_BOX.  
 FT DOMAIN 219 289 KRAB.  
 FT ZN\_FING 470 492 C2H2-TYPE 1.  
 FT ZN\_FING 498 520 C2H2-TYPE 2.  
 FT ZN\_FING 553 575 C2H2-TYPE 3.  
 FT ZN\_FING 581 604 C2H2-TYPE 4.  
 FT ZN\_FING 634 656 C2H2-TYPE 5.  
 FT ZN\_FING 662 686 C2H2-TYPE 6.  
 FT ZN\_FING 718 740 C2H2-TYPE 7.  
 FT ZN\_FING 746 768 C2H2-TYPE 8.  
 FT ZN\_FING 796 818 C2H2-TYPE 9.  
 FT ZN\_FING 824 846 C2H2-TYPE 10.  
 FT ZN\_FING 933 955 C2H2-TYPE 11.  
 FT ZN\_FING 961 983 C2H2-TYPE 12.  
 FT CONFLICT 495 495 V -> L (IN REF. 2; AAH34572).  
 FT CONFLICT 709 709 R -> Q (IN REF. 2; AAH34572).  
 SQ SEQUENCE 986 AA; 114774 MW; 28F5684634C32DFE CRC64;

Query Match 59.7%; Score 37; DB 1; Length 986;  
Best Local Similarity 77.8%; Pred. No. 56;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RQOELTKQ 10  
Db 45 RQOELFRQ 53

RESULT 15

2445 HUMAN STANDARD; PRT; 1031 AA.  
AC P59923;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Zinc finger protein 445.  
GN ZNF445 OR ZNF168.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shan Y.X., Luo K.T., Guo Z.K., Tang W.W., Ye G.M., Yu L., Huang C.Q.;  
RT "Cloning and characterization of a novel zinc finger protein."  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: May be involved in transcriptional regulation.  
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).  
CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.  
CC -!- SIMILARITY: Contains 1 KRAB domain.  
CC -!- SIMILARITY: Contains 1 SCAN box domain.  
CC -!- SIMILARITY: Contains 14 C2H2-type zinc fingers.  
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CC  
CC EMBL; AY262260; RAP36990.1; -;  
CC EMBL; AY295873; RAP50258.1; -;  
CC Genew; HGNC:21018; ZNF445.  
CC PROSITE; P50805; KRAB; 1.  
CC PROSITE; P50804; SCAN\_BOX; 1.  
CC PROSITE; P50028; ZINC\_FINGER\_C2H2\_1; 14.  
CC PROSITE; P50157; ZINC\_FINGER\_C2H2\_2; 14.  
CC Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;  
CC Nuclear protein; Repeat.  
CC DOMAIN 55 137  
CC FT DOMAIN 55 137  
CC FT ZN\_FING 234 304  
CC FT ZN\_FING 485 507  
CC FT ZN\_FING 513 535  
CC FT ZN\_FING 541 563  
CC FT ZN\_FING 597 619  
CC FT ZN\_FING 625 647  
CC FT ZN\_FING 681 703  
CC FT ZN\_FING 709 731  
CC FT ZN\_FING 762 784  
CC FT ZN\_FING 790 812  
CC FT ZN\_FING 840 862  
CC FT ZN\_FING 868 890  
CC FT ZN\_FING 896 918  
CC FT ZN\_FING 978 1000  
CC FT ZN\_FING 1006 1028  
CC FT ZN\_FING 1031 AA; 118962 MW; 39C288602894006E CRC64;  
CC SEQUENCE

Query Match 59.7%; Score 37; DB 1; Length 1031;  
Best Local Similarity 77.8%; Pred. No. 59;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RQOELTKQ 10  
Db 48 RQOELFRQ 56

RESULT 16

KCH8 RAT STANDARD; PRT; 1102 AA.  
AC Q9QWS8; O88877;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Potassium voltage-gated channel subfamily H member 8 (Ether-a-go-go-like potassium channel 3) (ELK channel 3).  
GN KCH8 OR ELK3 OR ELK1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=96382545; PubMed=9714851;  
RA Shi W., Wang H.-S., Pan Z., Wymore R.S., Cohen I.S., McKinnon D.,  
RT "Cloning of a mammalian elk potassium channel gene and EAG mRNA distribution in rat sympathetic ganglia."  
RL J. Physiol. (Lond) 511:675-682(1998).  
RN [2]  
RP SEQUENCE OF 9-379 FROM N.A.  
RC TISSUE=Brain cortex;  
RX MEDLINE=99043952; PubMed=9824707;  
RA Engeland B., Neu A., Ludwig J., Roeper J., Pongs O.;  
RT "Cloning and functional expression of rat ether-a-go-go-like K<sup>+</sup> channel genes."  
RL J. Physiol. (Lond) 513:647-654(1998).  
RN [3]  
RP TISSUE SPECIFICITY.  
RX MEDLINE=20183472; PubMed=10718922;  
RA Wulfsen I., Hauber H.-P., Schiemann D., Bauer C.K., Schwarz J.R.;  
RT "Expression of mRNA for voltage-dependent and inward-rectifying K<sup>+</sup> channels in GH3/36 cells and rat pituitary."  
RL J. Neuroendocrinol. 12:263-272(2000).  
RN [4]  
RP TISSUE SPECIFICITY.  
RX MEDLINE=21319165; PubMed=11425889;  
RA Saganich M.J., Machado E., Rudy B.;  
RT "Differential expression of genes encoding subthreshold-operating voltage-gated K<sup>+</sup> channels in brain."  
RL J. Neurosci. 21:4609-4624(2001).  
CC -!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium channel. Elicits a slowly activating, outward rectifying current.  
CC -!- SUBUNIT: The potassium channel is probably composed of a homo- or heterotetrameric complex of pore-forming alpha subunits that can associate with modulating beta subunits.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Detected in superior cervical, mesenteric and colonic ganglia. Expressed in brain (piriform cortex, olfactory tubercle, cerebral cortex, hippocampus pyramidal cells and dentate gyrus and basal ganglia of caudate/putamen and accumbens nucleus). Expressed in pituitary.  
CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.  
CC -!- SIMILARITY: Belongs to the potassium channel family. H (Eag) subfamily.  
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.  
CC -!- SIMILARITY: Contains 1 PAS (FER-ARNT-SIM) dimerization domain.  
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.  
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CC -----  
 CC EMBL: AF061957; AAC61520.1; .  
 CC EMBL: AJ007632; CAA07591.1; .  
 CC PIR: T17367; T17367; CNMP binding.  
 CC InterPro: IPR000595; CNMP binding.  
 CC InterPro: IPR003967; Erg\_channel.  
 CC InterPro: IPR005821; Ion\_trans.  
 CC InterPro: IPR001632; K+channel\_pore.  
 CC InterPro: IPR005820; M+channel\_nlg.  
 CC InterPro: IPR001610; PAC.  
 CC InterPro: IPR000700; PAS-assoc\_C.  
 CC InterPro: IPR000014; PAS\_domain.  
 CC Pfam: PF00027; CNMP\_binding; 1.  
 CC Pfam: PF00520; Ion\_trans; 1.  
 CC Pfam: PF00785; PAC; 1.  
 CC PRINTS: PR01470; ERGCHANNEL.  
 CC SMART: SM00100; CNMP; 1.  
 CC SMART: SM00086; PAC; 1.  
 CC TIGRFS: TIGR00229; sensory\_box; 1.  
 CC PROSITE: PS00888; CNMP\_BINDING\_1; FALSE\_NEG.  
 CC PROSITE: PS00889; CNMP\_BINDING\_2; FALSE\_NEG.  
 CC PROSITE: PS0042; CNMP\_BINDING\_3; 1.  
 CC PROSITE: PS0113; PAC; 1.  
 CC PROSITE: PS0112; PAS; FALSE\_NEG.

CC Transport; Ion transport; Ionic channel; Voltage-gated channel;  
 CC Potassium channel; Potassium; Potassium transport; Transmembrane;  
 CC Glycoprotein; Multigene family.  
 CC DOMAIN 1 225  
 CC CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 226 246  
 CC SEGMENT S1 (POTENTIAL).  
 CC TRANSMEM 256 276  
 CC SEGMENT S2 (POTENTIAL).  
 CC DOMAIN 277 298  
 CC CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 299 319  
 CC SEGMENT S3 (POTENTIAL).  
 CC TRANSMEM 328 348  
 CC SEGMENT S4 (POTENTIAL).  
 CC DOMAIN 349 353  
 CC CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 354 374  
 CC SEGMENT S5 (POTENTIAL).  
 CC DOMAIN 420 440  
 CC SEGMENT H5 (PORE-FORMING) (POTENTIAL).  
 CC TRANSMEM 449 469  
 CC SEGMENT S6 (POTENTIAL).  
 CC DOMAIN 470 1102  
 CC CYTOPLASMIC (POTENTIAL).  
 CC PAS.  
 CC DOMAIN 18 90  
 CC TRANSMEM 93 145  
 CC POLY-GLU.  
 CC DOMAIN 711 722  
 CC NP\_BIND 551 668  
 CC CARBOHYD 320 320  
 CC CARBOHYD 409 409  
 CC N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC F -> L (IN REF. 2).  
 CC K -> N (IN REF. 2).  
 CC I -> T (IN REF. 2).  
 CC M -> I (IN REF. 2).  
 CC CONFLICT 187 187  
 CC CONFLICT 296 296  
 CC CONFLICT 370 370  
 CC CONFLICT 370 370  
 CC SEQUENCE 1102 AA; 123230 MW; A135CC36E2E7F1A3 CRC64;

Query Match 59.7%; Score 37; DB 1; Length 1102;  
 Best Local Similarity 54.5%; Pred. No. 64;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 CRPQELTKQG 11  
 Db 572 CAPGEYLLRQG 582  
 |||:|:|  
 |::|:|:|

RESULT 17  
 ID\_KCH8\_HUMAN STANDARD; PRT; 1107 AA.  
 AC Q96L42;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Potassium voltage-gated channel subfamily H member 8 (Ether-a-go-go-  
 DE like potassium channel 3) (ELK3) (ELK1) (HEK1).

GN KCH8.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=21895915; PubMed=11897058;  
 RA Baxter D.F., Kirk M., Garcia A.F., Raimondi A., Holmqvist M.H.,  
 RA Flint K.K., Bojancic D., DiStefano P.S., Curtis R., Xie Y.;  
 RT "A novel membrane potential-sensitive fluorescent dye improves  
 RT cell-based assays for ion channels.";  
 RL J. Biol. Screen. 7:79-85 (2002).  
 CC -!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium  
 CC channel. Elicits a slowly activating, outward rectifying current.  
 CC Channel properties may be modulated by cAMP and subunit assembly.  
 CC -!- SUBUNIT: The potassium channel is probably composed of a homo- or  
 CC heterotetrameric complex of pore-forming alpha subunits that can  
 CC associate with modulating beta subunits.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is  
 CC characterized by a series of positively charged amino acids at  
 CC every third position.  
 CC -!- SIMILARITY: Belongs to the potassium channel family. H (Eag)  
 CC subfamily.  
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.  
 CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.  
 CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 CC EMBL: AY053503; AAL15429.1; .  
 CC Genes: HGNC:18864; KCH8.  
 CC InterPro: IPR000595; CNMP\_binding.  
 CC InterPro: IPR003967; Erg\_channel.  
 CC InterPro: IPR005821; Ion\_trans.  
 CC InterPro: IPR001622; K+channel\_pore.  
 CC InterPro: IPR005820; M+channel\_nlg.  
 CC InterPro: IPR001610; PAC.  
 CC InterPro: IPR000700; PAS-assoc\_C.  
 CC InterPro: IPR000014; PAS\_domain.  
 CC Pfam: PF00027; CNMP\_binding; 1.  
 CC Pfam: PF00520; Ion\_trans; 1.  
 CC Pfam: PF00785; PAC; 1.  
 CC PRINTS: PR01470; ERGCHANNEL.  
 CC SMART: SM00100; CNMP; 1.  
 CC SMART: SM00086; PAC; 1.  
 CC TIGRFS: TIGR00229; sensory\_box; 1.  
 CC PROSITE: PS00888; CNMP\_BINDING\_1; FALSE\_NEG.  
 CC PROSITE: PS00889; CNMP\_BINDING\_2; FALSE\_NEG.  
 CC PROSITE: PS0042; CNMP\_BINDING\_3; 1.  
 CC PROSITE: PS0113; PAC; 1.  
 CC PROSITE: PS0112; PAS; FALSE\_NEG.  
 CC Transport; Ion transport; Ionic channel; Voltage-gated channel;  
 CC Potassium channel; Potassium; Potassium transport; Transmembrane;  
 CC Glycoprotein; Multigene family.  
 CC DOMAIN 1 225  
 CC CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 226 246  
 CC SEGMENT S1 (POTENTIAL).  
 CC TRANSMEM 256 276  
 CC SEGMENT S2 (POTENTIAL).  
 CC DOMAIN 277 298  
 CC CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 299 319  
 CC SEGMENT S3 (POTENTIAL).  
 CC TRANSMEM 328 348  
 CC SEGMENT S4 (POTENTIAL).  
 CC DOMAIN 349 357  
 CC CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 358 378  
 CC SEGMENT S5 (POTENTIAL).  
 CC DOMAIN 420 440  
 CC SEGMENT H5 (PORE-FORMING) (POTENTIAL).  
 CC TRANSMEM 449 469  
 CC SEGMENT S6 (POTENTIAL).



DR	SWART; SW00179; EGF CA; 42.	
DR	PROSITE; PS00010; ASX HYDROXYL; 43.	
DR	PROSITE; PS00022; EGF_1; 2.	
DR	PROSITE; PS01186; EGF_2; 38.	
DR	PROSITE; PS00026; EGF_3; 45.	
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KW	Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;	
KW	Repeat; Signal; Multigene family.	
FT	SIGNAL 1 37	POTENTIAL.
FT	CHAIN 28 2871	FIBRILLIN 1.
FT	DOMAIN 81 112	EGF-LIKE 1.
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FT	DOMAIN 147 178	EGF-LIKE 3.
FT	DOMAIN 246 287	EGF-LIKE 4.
FT	DOMAIN 288 329	EGF-LIKE 5.
FT	DOMAIN 330 401	TGFBP 1.
FT	DOMAIN 402 445	PRO-RICH.
FT	DOMAIN 449 489	EGF-LIKE 6.
FT	DOMAIN 490 529	EGF-LIKE 7.
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FT	DOMAIN 572 612	EGF-LIKE 9.
FT	DOMAIN 613 653	EGF-LIKE 10.
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FT	DOMAIN 1363 1403	EGF-LIKE 23.
FT	DOMAIN 1404 1445	EGF-LIKE 24.
FT	DOMAIN 1446 1486	EGF-LIKE 25.
FT	DOMAIN 1487 1527	EGF-LIKE 26.
FT	DOMAIN 1528 1599	TGFBP 4.
FT	DOMAIN 1606 1647	EGF-LIKE 27.
FT	DOMAIN 1648 1688	EGF-LIKE 28.
FT	DOMAIN 1689 1758	TGFBP 5.
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FT	DOMAIN 1849 1890	EGF-LIKE 31.
FT	DOMAIN 1891 1929	EGF-LIKE 32.
FT	DOMAIN 1930 1972	EGF-LIKE 33.
FT	DOMAIN 1973 2012	EGF-LIKE 34.
FT	DOMAIN 2013 2054	EGF-LIKE 35.
FT	DOMAIN 2055 2121	TGFBP 6.
FT	DOMAIN 2122 2165	EGF-LIKE 36.
FT	DOMAIN 2166 2205	EGF-LIKE 37.
FT	DOMAIN 2206 2246	EGF-LIKE 38.
FT	DOMAIN 2247 2290	EGF-LIKE 39.
FT	DOMAIN 2291 2332	EGF-LIKE 40.
FT	DOMAIN 2333 2400	TGFBP 7.
FT	DOMAIN 2402 2443	EGF-LIKE 41.
FT	DOMAIN 2444 2484	EGF-LIKE 42.
FT	DOMAIN 2485 2523	EGF-LIKE 43.
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Query Match		59.7%;	Score 37; DB 1; Length 2871;
Best Local Similarity		54.5%;	Pred. No. 1.8e+02;
Matches	6; Conservative	1;	Mismatches 4; Indels 0; Gaps 0;
Qy	1 CRQCELTQKQ 11		
Db	1835 CKPGRLTSTG 1845		
RESULT 19			
PEXC ARATH			
ID_PEXC ARATH	STANDARD;	PRT;	372 AA.
AC	Q9M841;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Putative peroxisome assembly protein 12 (Peroxin-12).		
GN	AT3G04460 OR T27C4.11		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsi.		
OX	NCBI_TaxID=3702;		
RN	[1]		
RP	SEQUENCE FROM N. A.		
RC	STRAIN=cv. Columbia;		
RC	MEDLINE=21016720; PubMed=11130713;		
RA	Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseid M.,		
RA	Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermayer B.,		
RA	Delsen M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,		
RA	De Simone V., Choisine N., Artiguenave F., Robert C., Brotier P.,		
RA	Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,		
RA	Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,		
RA	Wiedemann R., Drzonek H., Erle H., Jordan R., Bangert S.,		
RA	Vezi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,		
RA	Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,		
RA	Reichert J., Scharfe M., Schoen O., Barques M., Terol J., Climent J.,		
RA	Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,		
RA	Cooke R., Laurie M., Berger-Liauro C., Purnelle B., Masuy D.,		
RA	de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,		
RA	Monfort A., Argitrou A., Flores M., Liguori R., Vitale D.,		
RA	Manthaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Meves H.-W.,		
RA	Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,		
RA	Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,		
RA	Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,		
RA	Pai G., Miltscher J., Sellers P., Gill J.E., Feldblyum T.V.,		
RA	Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,		
RA	Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,		
RA	Sasamoto S., Kohara T., Idesawa K., Kawashima K., Kishida Y.,		
RA	Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,		
RA	Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,		
RA	Watanabe A., Yamada M., Yasuda M., Tabata S.,		
RT	"Sequence and analysis of chromosome 3 of the plant Arabidopsis		
RT	thaliana."		
RL	Nature 408:820-822(2000).		
CC	-!- FUNCTION: Required for protein import into peroxisomes (By		
CC	similarity).		
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein. Peroxisomal		
CC	(Potential).		
CC	-!- SIMILARITY: Belongs to the peroxin 12 family.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	use by non-profit institutions as long as its content is in no way		
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>		
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).		

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DR EMBL; AC022287; AAR63777.1; -.
DR InterPro; IPR006845; Pex2_Pex12.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF04757; Pex2_Pex12; 1.
DR SMART; SM00184; RING; 1.
DR Hypothetical protein; Transmembrane; Peroxisome.
SQ SEQUENCE 372 AA; 41809 MW; 2ACAD119B27114A5 CRC64;
Query Match 58.9%; Score 36.5; DB 1; Length 372;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 CR-PGQELTKQG 11
DB 234 CRATGQELTKQG 245
RESULT 20
RS4_ANASP STANDARD; PRT; 202 AA.
AC QVYTIQ;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S4.
GN RPSD OR RPS4 OR ALR2737.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
CC directly to 16S rRNA where it nucleates assembly of the body of
CC the 30S subunit (By similarity).
CC -!- FUNCTION: With S5 and S12 plays an important role in translational
CC accuracy (By similarity).
CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts protein S5.
CC The interaction surface between S4 and S5 is involved in control
CC of translational fidelity (By similarity).
CC -!- SIMILARITY: Contains 1 S4 RNA-binding domain.
CC -!- SIMILARITY: Belongs to the S4P family of ribosomal proteins.
CC
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CC
CC EMBL; AP003590; BAB74436.1; -.
CC PIR; AB2148; AB2148.
CC HANAP; MF_01306; -.
CC InterPro; IPR001912; Ribosomal_S4.
CC InterPro; IPR005709; Ribosomal_S4_b/o.
CC Pfam; PF00163; Ribosomal_S4.
CC Pfam; PF01479; S4; 1.
CC SMART; SM00363; S4; 1.
CC TIGRFAMs; TIGR01017; rpsD_bact; 1.
CC PROSITE; PS00632; RIBOSOMAL_S4; 1.
CC PROSITE; PS00889; S4; 1.
KW Ribosomal protein; RNA-binding; rRNA-binding; Complete proteome.
FT DOMAIN 90 152
S4 RNA-BINDING.
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SQ SEQUENCE 202 AA; 23247 MW; E87CC650A4447229 CRC64;
Query Match 58.1%; Score 36; DB 1; Length 202;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRPGQEL 7
DB 131 CRPGEEI 137
RESULT 21
NCAP_VHSVO STANDARD; PRT; 404 AA.
ID NCAP_VHSVO
AC P24378;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DE Nucleocapsid protein (Nucleoprotein).
GN N.
OS Viral hemorrhagic septicemia virus (strain 07-71) (VHSV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Novirhabdovirus.
OX NCBI_TaxID=11288;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90362052; PubMed=2202782;
RA Bernard J., Lecocq-Xhonneux F., Rossius M., Thiry M.E.,
RA de Kinkelin P.;
RT "Cloning and sequencing the messenger RNA of the N gene of viral
haemorrhagic septicemia virus."
RL J. Gen. Virol. 71:1669-1674(1990).
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: TO HNVP NUCLEOCAPSID PROTEIN.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sb-sib.ch).
CC
CC EMBL; D00687; BAA00591.1; -.
CC PIR; A36651; VHVNS.
CC InterPro; IPR004902; Rhabdo_ncap_2.
CC Pfam; PF03216; Rhabdo_ncap_2; 1.
CC Nucleocapsid; Phosphorylation.
SQ SEQUENCE 404 AA; 44369 MW; 6C7200217ABA33A4 CRC64;
Query Match 58.1%; Score 36; DB 1; Length 404;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 RFGQELTK 9
DB 184 RFGQKITK 191
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ID NCAP_VHSVM
AC P27371;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Nucleocapsid protein (Nucleoprotein).
GN N.
OS Viral hemorrhagic septicemia virus (strain Makah) (VHSV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Novirhabdovirus.
OX NCBI_TaxID=11289;
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=92341050; PubMed=1634868;
RA Bernard J., Bremont M., Winton J.;
RT "Nucleocapsid gene sequence of a North American isolate of viral
RL J. Gen. Virol. 73:1011-1014(1992).
CC -1- PTM: Phosphorylated.
CC -1- SIMILARITY: TO INHV NUCLEOCAPSID PROTEIN.
CC -----
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CC -----
DR EMBL; X59241; CAA41930.1; -.
DR PIR; JQ1531; JQ1531.
DR InterPro; IPR004902; Rhabdo_ncap_2.
DR Pfam; PF03216; Rhabdo_ncap_2; 1.
KW Nucleocapsid; Phosphorylation.
SQ SEQUENCE 404 AA; 44066 MW; 54505A3455646DA1 CRC64;

Query Match 58.1%; Score 36; DB 1; Length 404;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 RFGQLTK 9
DB 184 RFGQKITK 191

RESULT 23
EPB2_CHICK STANDARD; PRT; 1004 AA.
AC P28693;
DT 01-DEC-1992 (Rel. 24, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ephrin type-B receptor 2 precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor CEK5).
GN EPB2 OR CEK5.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC TISSUE=Embryo;
RX MEDLINE=92144672; PubMed=1664238;
RA Pasquale E.B.;
RT "Identification of chicken embryo kinase 5, a developmentally
RT regulated receptor-type tyrosine kinase of the Eph family."
RL Cell Regul. 2:523-534(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC TISSUE=Brain;
RX MEDLINE=93288394; PubMed=8510926;
RA Sajjadi F.G., Pasquale E.B.;
RT "Five novel avian Eph-related tyrosine kinases are differentially
RT expressed".
RL Oncogene 8:1807-1813(1993).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. PROBABLY AN
CC IMPORTANT COMPONENT OF SIGNAL TRANSDUCTION PATHWAYS.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=long; Synonyms=CEK5+;
CC IsoId=P28693-1; Sequence=Displayed;

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CC Name=Short;
CC IsoId=P28693-2; Sequence=VSP_003018;
CC -1- TISSUE SPECIFICITY: WIDE TISSUE DISTRIBUTION THROUGHOUT
CC DEVELOPMENT AND SUSTAINED EXPRESSION IN ADULT BRAIN. THE LONGER
CC FORM (CEK5+) IS SPECIFICALLY EXPRESSED IN THE CENTRAL NERVOUS
CC SYSTEM.
CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
CC receptor subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M62325; AAA48667.1; ALT_INIT.
DR PDB; 1SGG; 06-OCT-99.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001090; Ephrin_receptor.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003962; FN_III subd.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR001426; Ykase_receptorV.
DR Pfam; PF01404; EPH_1bd; 1.
DR Pfam; PF00041; fn3_2.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00536; SAM; 1.
DR PRINTS; PR00014; FNTYPEIII.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD001495; Ephrin_receptor; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00615; EPH_1bd; 1.
DR SMART; SM00060; FN3_2.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00219; TyrcK; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS0105; SAM_DOMAIN; 1.
DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
DR Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing;
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 1004 EPHRIN TYPE-B RECEPTOR 2.
FT DOMAIN 20 544 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 545 565 POTENTIAL.
FT DOMAIN 566 1004 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 20 321 CYS-RICH.
FT DOMAIN 326 419 FIBRONECTIN TYPE-III 1.
FT DOMAIN 437 521 FIBRONECTIN TYPE-III 2.
FT DOMAIN 639 902 PROTEIN KINASE.
FT DOMAIN 931 935 SAM.
FT SITE 1002 1004 PDZ-BINDING MOTIF (POTENTIAL).
FT NP_BIND 645 653 ATP (BY SIMILARITY).
FT BINDING 671 671 ATP (BY SIMILARITY).
FT ACT_SITE 764 764 BY SIMILARITY.
FT MOD_RES 614 614 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 620 620 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 798 798 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 948 948 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 266 266 N-LINKED (GLCNAC...) (POTENTIAL).

```

SMART: SM00404; PTPC\_motif: 1.  
PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
PROSITE; PSS0056; TYR\_PHOSPHATASE\_2; FALSE\_NEG.  
Hydrolase.  
ACT\_SITE 413 413 PROSPHOCYSTEINE INTERMEDIATE (BY  
SIMILARITY).  
SEQUENCE 1075 AA; 120225 MW; 2FDDE124B9515F29 CRC64;  
Query Match 58.1%; Score 36; DB 1; Length 1075;  
Best Local Similarity 50.0%; Pred. No. 96;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY |||||:  
DB 151 CRGGEHWTSR 160  
RESULTS 25  
MTR3 HUMAN  
ID MTR3 HUMAN STANDARD; PRT; 1198 AA.  
Q13615; Q9NYN5; Q9NYN6; Q9UDX6; Q9UEG3;  
01-NOV-1997 (Rel. 35, Created)  
10-OCT-2003 (Rel. 42, Last sequence update)  
10-OCT-2003 (Rel. 42, Last annotation update)  
Myotubularin-related protein 3 (EC 3.1.3.48) (FYVE domain-containing  
dual specificity protein phosphatase 1) (FYVE-DSPI).  
MTRW3 OR KIAA0371.  
Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
SEQUENCE FROM N.A. (ISOFORMS A; B AND C), AND CHARACTERIZATION.  
MEDLINE=20000121; PubMed=10733931;  
Zhao R., Qi Y., Zhao Z.J.;  
"FYVE-DSPI, a dual-specificity protein phosphatase containing an FYVE  
domain.";  
Biochem. Biophys. Res. Commun. 270:222-229 (2000).  
[2]  
SEQUENCE FROM N.A. (ISOFORM B).  
TIGSUF=Brain;  
MEDLINE=97349984; PubMed=9205841;  
Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,  
Miyaajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
"Prediction of the coding sequences of unidentified human genes. VII.  
The complete sequences of 100 new cDNA clones from brain which can  
code for large proteins in vitro";  
DNA Res. 4:141-150 (1997).  
[3]  
SEQUENCE FROM N.A.  
MEDLINE=20057165; PubMed=10591208;  
Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,  
Almeida J.P., Babbage A.K.,  
Clamp M., Smink L.J., Ainscough R.F., Bates K.N., Beasley O.P.,  
Bagnoley C., Bailey J., Barcough K.F., Buck D., Burgess J.,  
Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burch J.,  
Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,  
Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,  
Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,  
Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,  
Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,  
Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,  
Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,  
Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,  
Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,  
Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,  
McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,  
Odeli C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,  
Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,  
Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,  
Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,  
Vaadin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,  
Williams L., Williams S.A., Williamson H., Wilner T.E., Wilming L.,  
Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,

RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,  
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,  
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,  
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,  
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,  
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,  
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,  
RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,  
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,  
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,  
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,  
RA Scheet P., Walker C., Wansley A., Wohlmann P., Pepin K., Nelson J.,  
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,  
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,  
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,  
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,  
RA Peyrard M., Kedra D., Seroussi E., Franssion I., Tapia I., Bruder C.E.,  
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,  
RA Khan A.S., Lane L., Tilahun Y., Wright H.,  
RT "The DNA sequence of human chromosome 22.";  
RL Nature 402:489-495(1999).  
RN [4]  
RP SEQUENCE OF 374-578 FROM N.A.  
RX MEDLINE=98409499; PubMed=9736772;  
RA Laporte J., Blondeau F., Buj-Bello A., Tentler D., Kretz C., Dahl N.,  
RA Mandel J.-L.;  
RT "Characterization of the myotubularin dual specificity phosphatase  
RT gene family from yeast to human.";  
RL Hum. Mol. Genet. 7:1703-1712(1998).  
RN [5]  
RP SEQUENCE OF 381-463 FROM N.A.  
RX MEDLINE=96225444; PubMed=8640223;  
RA Laporte J., Hu L.J., Kretz C., Mandel J.-L., Kioschis P., Coy J.,  
RA Klauk S.M., Poutska A., Dahl N.;  
RT "A gene mutated in X-linked myotubular myopathy defines a new  
RT putative tyrosine phosphatase family conserved in yeast.";  
RL Nat. Genet. 13:175-182(1996).  
CC -!- FUNCTION: Dephosphorylates proteins phosphorylated on Ser, Thr,  
CC and Tyr residues and low molecular weight phosphatase substrate  
CC para-nitrophenylphosphate.  
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
CC tyrosine + phosphate.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Name=B; Synonyms=FYVE-DSPIb;  
CC IsoId=Q13615-1; Sequence=Displayed;  
CC Name=A; Synonyms=FYVE-DSPIa;  
CC IsoId=Q13615-2; Sequence=VSP\_007781, VSP\_007782;  
CC Name=C; Synonyms=FYVE-DSPIc;  
CC IsoId=Q13615-3; Sequence=VSP\_007781;  
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-  
CC TYROSINE PHOSPHATASE FAMILY. MYOTUBULARIN SUBFAMILY.  
CC -!- SIMILARITY: Contains 1 FYVE-type zinc finger.  
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CC -----  
CC EMBL; AF233436; AAF40203.2; -;  
CC EMBL; AF233437; AAF40204.1; -;  
CC EMBL; AF233438; AAF40205.1; -;  
CC EMBL; AB002369; BAA20826.1; -;  
CC EMBL; AC003071; AAB83949.1; -;  
CC EMBL; U58034; AAC79119.1; -;  
CC Genew; HGNC:7451; MTR3.  
CC MIM; 603558; -;  
CC DR GO:0005737; C:cytoplasm; TAS.  
CC DR GO:0016020; C:membrane; TAS.  
CC GO:0016020; C:membrane; TAS.

DR GO:0004725; F:protein tyrosine phosphatase activity; TAS.  
DR GO:0008138; F:protein tyrosine/threonine phosphatase...; TAS.  
DR GO:0006470; P:protein amino acid dephosphorylation; TAS.  
DR InterPro: IPR003595; PTPC motif.  
DR InterPro: IPR000387; TYR\_Posphatase.  
DR InterPro: IPR000306; Znf\_FYVE.  
DR Pfam; PF01363; FYVE; 1.  
DR SMART; SMO0064; FYVE; 1.  
DR SMART; SMO0404; PTPC.motif; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
DR PROSITE; PS00556; TYR\_PHOSPHATASE\_2; FALSE\_NEG.  
DR PROSITE; PS0178; ZF\_FYVE; 1.  
KW Hydrolase; Zinc-finger; Alternative splicing.  
FT ZN\_FING 1119 1179  
FT ACT\_SITE 413 413  
FT VARSPLIC 1076 1112  
FT Missing (in isoform A and isoform C).  
FT /FTID=VSP\_007781.  
FT R -> RDTDRVDQTW (in isoform A).  
FT /FTID=VSP\_007782.  
FT LYPVCHVRNMLWSAVLP -> CILQPHCQQQKEFGVGV  
FT I (IN REF. 4).  
SQ SEQUENCE 1198 AA; 133618 MW; FE6F4B165074D5F8 CRC64;  
Query Match 58.1%; Score 36; DB 1; Length 1198;  
Best Local Similarity 50.0%; Pred. No. 1.1e-02;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 CRPGQELTKQ 10  
Db 151 CRPGEHVTSR 160  
RESULT 26  
ATPZ\_VIBAL STANDARD; PRT; 129 AA.  
ID ATPZ\_VIBAL  
AC P12983;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE ATP synthase protein I.  
GN ATP1 OR UNCL.  
OS Vibrio alginolyticus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
CX NCBI\_TaxID=663;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=138-2;  
RX MEDLINE=90016889; PubMed=2529481;  
RA Krumholz L.R., Esser U., Simoni R.D.;  
RT "Nucleotide sequence of the unc operon of Vibrio alginolyticus.";  
RL Nucleic Acids Res. 17:7993-7994(1989).  
CC -!- FUNCTION: A possible function for this protein is to guide the  
CC assembly of the membrane sector of the ATPase enzyme complex.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
CC (Potential).  
CC -!- SIMILARITY: TO THE CORRESPONDING SUBUNIT IN OTHER BACTERIA.  
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CC -----  
CC EMBL; X16050; CAA34174.1; -;  
CC PIR; S06075; S06075.  
CC InterPro: IPR005598; ATP\_synth\_I.  
CC Pfam; PF03899; ATP\_synth\_I; 1.  
CC KW Hydrogen ion transport; CF(0); Transmembrane; Inner membrane.  
CC TRANSMEM 16 36  
CC POTENTIAL.

FT TRANSNM 44 64 POTENTIAL.  
 FT TRANSNM 77 97 POTENTIAL.  
 FT TRANSNM 105 125 POTENTIAL.  
 SQ SEQUENCE 129 AA; 13835 MW; E376666CC1BE6C10 CRC64;  
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 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 RPQELTKQ 10  
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 Db 7 RRGELARQ 15  
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 RESULT 27  
 ECHC MYCTU STANDARD; PRT; 285 AA.  
 AC OS3163;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Probable enoyl-CoA hydratase echa12 (EC 4.2.1.17).  
 GN ECHA12 OR FADH2 OR RV1472 OR MT1518 OR MTW007.19.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 Gordon S.V., Eiglemer K., Gas S., Barry C.E. III, Tekala F.,  
 Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,  
 Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 Rutter S., Seeger K., Skelton S., Squares R., Squares R.,  
 Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;  
 RT Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence."  
 RL Nature 393:537-544 (1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RX MEDLINE=22206494; PubMed=12218036;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,  
 Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,  
 Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;  
 RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains."  
 RL J. Bacteriol. 184:5479-5490 (2002).  
 CC -1- FUNCTION: COULD POSSIBLY OXIDIZES FATTY ACIDS USING SPECIFIC  
 CC COMPONENTS (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: (3S)-3-hydroxyacyl-CoA = trans-2(or 3)-enoyl-  
 CC CoA + H(2)O.  
 CC -1- SIMILARITY: Belongs to the enoyl-CoA hydratase/isomerase family.  
 CC  
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 CC  
 DR EMBL; AL021184; CAA16000.1; -  
 DR EMBL; AE007021; AAK45783.1; -  
 DR PIR; C70873; C70873.  
 DR HGSP; P14604; 2DUB.  
 DR TIGR; MT1518; -

DR Tuberculin; RV1472; -  
 DR InterPro; IPR001753; EnCoA\_hydrase.  
 DR Pfam; PF00378; ECH; 1.  
 DR PROSITE; PS00166; ENOYL COA HYDRATASE; 1.  
 KW Fatty acid metabolism; Lyase; Complete proteome.  
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 Query Match 56.5%; Score 35; DB 1; Length 285;  
 Best Local Similarity 77.8%; Pred.No. 35;  
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 QY 2 RPQELTKQ 10  
 |||||:  
 Db 226 RRGELTKR 234  
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 RESULT 28  
 NU2M ONCMY STANDARD; PRT; 349 AA.  
 AC P48175;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).  
 GN MTND2 OR ND2.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=96139027; PubMed=85871139;  
 RA Zardoya R., Garrido-Petier A., Bautista J.M.;  
 RT "The complete nucleotide sequence of the mitochondrial DNA genome of  
 RT the rainbow trout, Oncorhynchus mykiss."  
 RL J. Mol. Evol. 41:942-951 (1995).  
 CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- SIMILARITY: Belongs to the complex I subunit 2 family.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; L29771; AAB03348.1; -  
 DR PIR; T09858; T09858.  
 DR InterPro; IPR003917; NADHoxred2.  
 DR InterPro; IPR001750; Oxidored\_q1.  
 DR Pfam; PF00361; oxidored\_q1; 1.  
 DR PRINTS; PR01436; NADHGHGASE2.  
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.  
 SQ SEQUENCE 349 AA; 37797 MW; 877DC34A237DADDF CRC64;  
 Query Match 56.5%; Score 35; DB 1; Length 349;  
 Best Local Similarity 100.0%; Pred.No. 44;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 QELTKQG 11  
 |||||:  
 Db 268 QELTKQG 274  
 |||||:  
 RESULT 29  
 NU2M SALSA STANDARD; PRT; 349 AA.  
 ID NU2M SALSA

AC Q35924: Q9MPEG9;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).  
 GN MTND2 OR ND2 OR NADH2 OR NADH-2.  
 OS Salmo salar (Atlantic salmon).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.  
 OX NCBI\_TaxID=8030;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=20018174; PubMed=10548724;  
 RA Hurst C.D., Bartlett S.E., Davidson W.S., Bruce I.J.;  
 RT "The complete mitochondrial DNA sequence of the Atlantic salmon, *Salmo salar*,"  
 RL Gene 239:237-242(1999).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RA Arnason U., Johnsson E., Rasmussen A.S.;  
 RT "The complete mitochondrial genome sequence of a teleost, *Salmo salar*, and comparisons with other salmoniformes,"  
 RL submitted (MAR-1999) to the EMBL/GenBank/DBP databases.  
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.  
 CC -!- SIMILARITY: Belongs to the complex I subunit 2 family.  
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 CC  
 CC EMBL; U12143; AAD04734.1; -;  
 CC EMBL; AF133701; AAF61379.1; -;  
 CC PIR; T09948; T09948.  
 CC InterPro; IPR003917; NADHub\_oxred2.  
 CC InterPro; IPR001750; Oxidored\_g1.  
 CC Pfam; F00361; oxidored\_g1; 1.  
 CC PRINTS; PR01436; NADHGNASE2.  
 CC Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.  
 FT CONFLICT 79 79 W -> R (IN REF. 2).  
 SQ SEQUENCE 349 AA; 37853 MW; 1690A416D81B5358 CRC64;  
 Query Match 56.5%; Score 35; DB 1; Length 349;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 QELTKQG 11  
 |||||  
 DB 266 QELTKQG 274  
 RESULT 30  
 ARGD THEME  
 ID ARGD THEME STANDARD; PRT; 385 AA.  
 AC Q9X2A5;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Acetylornithine aminotransferase (EC 2.6.1.11) (ACOAT).  
 GN ARGD OR TM1785.  
 OS Thermotoga maritima.  
 OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.  
 OX NCBI\_TaxID=2336;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=MSB8 / DSM 3109 / ATCC 43589;  
 RX MEDLINE=99287316; PubMed=10360571;  
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Bisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;  
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of *Thermotoga maritima*,"  
 RL Nature 391:323-329(1999).  
 CC -!- CATALYTIC ACTIVITY: N(2)-acetyl-L-ornithine + 2-oxoglutarate = N-acetyl-L-glutamate 5-semialdehyde + L-glutamate.  
 CC -!- COFACTOR: Pyridoxal phosphate (By similarity).  
 CC -!- PATHWAY: Arginine biosynthesis, fourth step.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
 CC -!- MISCELLANEOUS: May also have succinylidiaminopimelate aminotransferase activity, thus carrying out the fourth step in lysine biosynthesis.  
 CC -!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent aminotransferases.  
 CC  
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 CC  
 CC EMBL; AE001816; AAD36848.1; -;  
 CC PIR; D72211; D72211.  
 CC HSP; P04181; ZOAT.  
 CC TIGR; TM1785; -;  
 CC HAMAP; MF\_01107; -; 1.  
 CC InterPro; IPR005814; Aminotrans\_3.  
 CC InterPro; IPR004636; Argp.  
 CC Pfam; PF00202; aminotran\_3; 1.  
 CC TIGRFAM; TIGR00707; argp; 1.  
 CC PROSITE; PS00600; AA\_TRANSFER\_CLASS\_3; 1.  
 CC Arginine biosynthesis; Transferase; Aminotransferase;  
 KW Pyridoxal phosphate; Complete proteome.  
 FT BINDING 240 240 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 SQ SEQUENCE 385 AA; 42884 MW; 4018F87FCB8FF0 CRC64;  
 Query Match 56.5%; Score 35; DB 1; Length 385;  
 Best Local Similarity 53.3%; Pred. No. 49;  
 Matches 8; Conservative 2; Mismatches 1; Indels 4; Gaps 1;  
 QY 1 CRPG---QELTKQG 11  
 |||||  
 DB 276 CRAGTVIKELTKG 290  
 RESULT 31  
 CIR\_HUMAN  
 ID CIR\_HUMAN STANDARD; PRT; 705 AA.  
 AC P00736;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Complement C1r component precursor (EC 3.4.21.41).  
 GN C1R  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87026566; PubMed=3021205;  
 RA Leytus S.P., Kurachi K., Sakariassen K.S., Davie E.W.;  
 RT "Nucleotide sequence of the cDNA coding for human complement C1r,"  
 RL Biochemistry 25:4855-4863(1986).



[2]  
SEQUENCE FROM N.A., AND VARIANT LEU-152.  
MEDLINE=87156625; PubMed=3030286;  
Journet A., Tosi M.;  
"Cloning and sequencing of full-length cDNA encoding the precursor of  
human complement component C1r.";  
Biochem. J. 240:783-787(1986).  
[3]  
SEQUENCE OF 18-463.  
MEDLINE=87241248; PubMed=3036070;  
Arlaud G.J., Willis A.C., Gagnon J.;  
"Complete amino acid sequence of the A chain of human complement-  
classical-pathway enzyme C1r.";  
Biochem. J. 241:711-720(1987).  
[4]  
SEQUENCE OF 464-705.  
MEDLINE=83204782; PubMed=6303394;  
Arlaud G.J., Gagnon J.;  
"Complete amino acid sequence of the catalytic chain of human  
complement subcomponent C1-r.";  
Biochemistry 22:1758-1764(1983).  
[5]  
SEQUENCE OF 152-186, AND HYDROXYLATION.  
MEDLINE=88005128; PubMed=2820791;  
Arlaud G.J., van Dorselaer A., Bell A., Mancini M., Aude C.,  
Gagnon J.;  
"Identification of erythro-beta-hydroxyasparagine in the EGF-like  
domain of human C1r.";  
FEBS Lett. 222:129-134(1987).  
[6]  
SEQUENCE OF 133-137; 187-211 AND 609-613, AND PHOSPHORYLATION.  
MEDLINE=86221263; PubMed=8635594;  
Felloux S., Thelens N.M., Hudry-Clergeon G., Petillot Y., Filhol O.,  
Arlaud G.J.;  
"Identification of a cryptic protein kinase CK2 phosphorylation site  
in human complement protease C1r, and its use to probe intramolecular  
interaction.";  
FEBS Lett. 386:15-20(1996).  
[7]  
STRUCTURE BY NMR OF 140-192.  
MEDLINE=98138432; PubMed=9477945;  
Bersch B., Hernandez J.-F., Marion D., Arlaud G.J.;  
"Solution structure of the epidermal growth factor (EGF)-like module  
of human complement protease C1r, an atypical member of the EGF  
family.";  
Biochemistry 37:1204-1214(1998).  
CC -1- FUNCTION: C1r B chain is a serine protease that combines with C1q  
and C1s to form C1, the first component of the classical pathway  
of the complement system.  
CC -1- CATALYTIC ACTIVITY: Selective cleavage of Lys(or Arg)-|-Ile bond  
in complement subcomponent C1s to form the active form of C1s  
(EC 3.4.21.42).  
CC -1- SUBUNIT: C1 is a calcium-dependent trimolecular complex of C1q,  
C1r and C1s in the molar ratio of 1:2:2. C1r is a dimer of  
identical chains, each of which is activated by cleavage into two  
chains, A and B, connected by disulfide bonds.  
CC -1- SIMILARITY: Belongs to peptidase family S1.  
CC -1- SIMILARITY: Contains 2 CUB domains.  
CC -1- SIMILARITY: Contains 1 EGF-like domain.  
CC -1- SIMILARITY: Contains 2 Sushi (SCR) domains.  
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CC EMBL; X04701; CAA28407.1; -;  
CC EMBL; M14058; AAA51851.1; -;  
CC PIR; A24170; C1HURB  
CC PDB; 1APQ; 17-SEP-97.

PDB; 1GPZ; 31-JUL-02.  
DR MEROPS; S01.192; -;  
DR Genew; HGNC:1246; C1r.  
DR MIM; 216950; -;  
DR GO; GO:0003815; F:complement component C1r activity; TAS.  
DR GO; GO:0008236; F:serine-type peptidase activity; TAS.  
DR GO; GO:0006955; P:immune response; TAS.  
DR InterPro; IPR000152; Asx\_Hydroxyl\_S.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
DR Pfam; PF00431; CUB; 2.  
DR Pfam; PF00084; sushi; 2.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PS00722; CHYMOTRYPSIN.  
DR SMART; SM00032; CCP; 2.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS001010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS01180; CUB; 2.  
DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
DR Complement pathway; Plasma; Glycoprotein; Serine protease; Hydrolase;  
KW Hydroxylation; Phosphorylation; Sushi; Repeat; Signal;  
KW EGF-like domain; 3D-structure; Polymorphism.  
FT SIGNAL 1 17  
FT CHAIN 18 463 COMPLEMENT C1R HEAVY CHAIN.  
FT CHAIN 464 705 COMPLEMENT C1R LIGHT CHAIN.  
FT DOMAIN 18 141 CUB 1.  
FT DOMAIN 142 190 EGF-LIKE, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 193 305 CUB 2.  
FT DOMAIN 308 372 SUSHI 1.  
FT DOMAIN 375 448 SUSHI 2.  
FT DOMAIN 464 705 SERINE PROTEASE.  
FT ACT\_SITE 502 502 CHARGE RELAY SYSTEM.  
FT ACT\_SITE 557 557 CHARGE RELAY SYSTEM.  
FT ACT\_SITE 654 654 CHARGE RELAY SYSTEM.  
FT MOD\_RES 157 167 HYDROXYLATION.  
FT MOD\_RES 206 206 PHOSPHORYLATION (BY CK2).  
FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .).  
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .).  
FT CARBOHYD 514 514 N-LINKED (GLCNAC. . .).  
FT CARBOHYD 581 581 N-LINKED (GLCNAC. . .).  
FT DISULFID 71 89 PROBABLE.  
FT DISULFID 146 165 PROBABLE.  
FT DISULFID 161 174 PROBABLE.  
FT DISULFID 176 189 PROBABLE.  
FT DISULFID 193 220 PROBABLE.  
FT DISULFID 250 268 PROBABLE.  
FT DISULFID 309 358 PROBABLE.  
FT DISULFID 338 371 PROBABLE.  
FT DISULFID 376 429 PROBABLE.  
FT DISULFID 406 447 PROBABLE.  
FT DISULFID 451 577 INTERCHAIN (PROBABLE).  
FT DISULFID 620 639 POTENTIAL.  
FT DISULFID 650 680 POTENTIAL.  
FT VARIANT 152 152 S -> L (in dbSNP:1801046).  
FT TURN 145 147 /FTID=VAR\_016103.  
FT TURN 150 152  
FT TURN 160 161  
FT TURN 164 168  
FT TURN 169 170  
FT STRAND 171 175

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FT TURN 178 179
FT STRAND 181 182
FT TURN 184 185
FT STRAND 189 190
SQ SEQUENCE 705 AA; 80173 MW; 5CBCC0201061463 CRC64;

Query Match 56.5%; Score 35; DB 1; Length 705;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQEL 7
DB 176 CRPGYEL 182

RESULT 32
MCM2 DROME
ID MCM2 DROME STANDARD; PRT; 887 AA.
AC P49735; Q9VHU2;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE DNA replication licensing factor MCM2.
GN MCM2 OR CG7538.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eve-antennal disk;
RX MEDLINE=93347580; PubMed=7622035;
RA Treisman J.E., Follette P.J., O'Farrell P.H., Rubin G.M.;
RT "Cell proliferation and DNA replication defects in a Drosophila MCM2
mutant.";
RL Genes Dev. 9:1709-1715(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Bueck H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissman J.J.,

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RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: Acts as a factor that allows the DNA to undergo a single
CC round of replication per cell cycle. Required for DNA replication
CC and cell proliferation.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: Belongs to the MCM family.
CC
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CC
CC -----
CC EMBL; L42762; AAB36617.1; -
CC EMBL; AE003678; AAF54207.1; -
CC FlyBase; FBgn0014861; MCM2.
CC InterPro; IPR001208; MCM.
CC InterPro; IPR008045; MCM_2.
CC Pfam; PF00493; MCM; 1.
CC PRINTS; PR01657; MCMFAMILY.
CC PRINTS; PR01658; MCMPROTEIN2.
CC ProDom; PD001041; MCM; 1.
CC SMART; SM00350; MCM; 1.
CC PROSITE; PS00847; MCM_1; 1.
CC PROSITE; PS00551; MCM_2; 1.
CC Transcription regulation; DNA-binding; Nuclear protein;
KW DNA replication; Zinc-finger; ATP-binding; Cell cycle.
FT ZN FING 314 340 C4-TYPE (POTENTIAL).
FT DOMAIN 458 665 MCM.
FT NP BIND 508 515 ATP (POTENTIAL).
SQ SEQUENCE 887 AA; 100414 MW; 26A7092109F09CBE CRC64;

Query Match 56.5%; Score 35; DB 1; Length 887;
Best Local Similarity 54.5%; Pred. No. 12e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
DB 391 CRPGDELEVTG 401

RESULT 33
RPOB BUCAP
ID RPOB BUCAP STANDARD; PRT; 1342 AA.
AC P41184;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase
DE beta chain) (RNA polymerase beta subunit).
GN RPOB OR BUSG035.
OS Buchnera aphidicola (subsp. Schizaphis graminum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=98794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93160925; PubMed=1369199;
RA Clark M.A., Baumann L., Baumann P.;
RT "Sequence analysis of an aphid endosymbiont DNA fragment containing
RT rpoB (beta-subunit of RNA polymerase) and portions of rplL and rpoC.";
RL Curr. Microbiol. 25:283-290(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22084549; PubMed=12089438;
RA Tamas I., Klason L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,

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RA Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;  
RT "50 million years of genomic stasis in endosymbiotic bacteria."  
RL Science 296:2376-2379(2002).  
CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription  
CC of DNA into RNA using the four ribonucleoside triphosphates as  
CC substrates.  
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
CC (RNA) (N).  
CC -!- SUBUNIT: The enzyme consists of the sigma chain and the core  
CC enzyme which is composed of 2 alpha chains, 1 beta chain, and 1  
CC beta' chain.  
CC -!- SIMILARITY: Belongs to the RNA polymerase beta chain family.  
CC  
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CC  
CC EMBL; Z11913; CAA77970.1; -.  
CC EMBL; AE014079; AAM67606.1; -.  
CC PIR; S32680; S32680.  
CC HSSP; Q9XWU7; 1HOM.  
CC InterPro; IPR007121; RNA\_pol\_B.  
CC InterPro; IPR007644; RNA\_pol\_Rpb2\_1.  
CC InterPro; IPR007642; RNA\_pol\_Rpb2\_2.  
CC InterPro; IPR007645; RNA\_pol\_Rpb2\_3.  
CC InterPro; IPR007120; RNA\_pol\_Rpb2\_6.  
CC InterPro; IPR007641; RNA\_pol\_Rpb2\_7.  
CC Pfam; PF04563; RNA\_pol\_Rpb2\_1; 1.  
CC Pfam; PF04561; RNA\_pol\_Rpb2\_2; 1.  
CC Pfam; PF04565; RNA\_pol\_Rpb2\_3; 1.  
CC Pfam; PF00562; RNA\_pol\_Rpb2\_6; 1.  
CC Pfam; PF04560; RNA\_pol\_Rpb2\_7; 1.  
CC PROSITE; PS01166; RNA\_POL\_BETA; 1.  
CC Transferase; Transcription; DNA-directed RNA polymerase;  
CC Complete proteome.  
CC  
CC SEQUENCE 1342 AA; 152060 MW; 7E30BC9E013D31ED CRC64;  
Query Match 56.5%; Score 35; DB 1; Length 1342;  
Best Local Similarity 66.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 2 RPOGLTKQ 10  
DB 371 RRGRLTKE 379  
RESULT 34  
ID TENS CHICK STANDARD; PRT; 1744 AA.  
AC Q04205; Q91007; Q92011.  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Tensin.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
EX MEDLINE=94350987; PubMed=8071358;  
RA Lo S.H., An Q., Bao S., Wong W.K., Liu Y., Jamney P.A., Hartwig J.H.,  
RA Chen L.B.;  
RT "Molecular cloning of chick cardiac muscle tensin. Full-length cDNA  
RT sequence, expression, and characterization."  
RL J. Biol. Chem. 269:22310-22319(1994).  
RN (2)

RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RX MEDLINE=95204530; PubMed=7896874;  
RA Chuang J.Z., Lin D.C., Lin S.;  
RT "Molecular cloning, expression, and mapping of the high affinity  
RT actin-capping domain of chicken cardiac tensin."  
RL J. Cell Biol. 128:1095-1109(1995).  
RN (3)  
RP SEQUENCE FROM N.A.  
RC Chen L.B.;  
RA Submitted (XX-1991) to the EMBL/GenBank/DBJ databases.  
RN (4)  
RP SEQUENCE OF 1469-1744 FROM N.A.  
RC TISSUE=Embryonic chondrocytes, and Embryonic heart;  
RX MEDLINE=94039118; PubMed=8223621;  
RA van de Werken R., Gemari M., Favella S., Bet P., Molina F.,  
RA Lin S., Canceda R., Castagnola P.;  
RT "Modulation of tensin and vimentin expression in chick embryo  
RT developing cartilage and cultured differentiating chondrocytes."  
RL Eur. J. Biochem. 217:781-790(1993).  
RN (5)  
RP SH2 DOMAIN.  
RX MEDLINE=91220073; PubMed=1708917;  
RA Davis S., Lu M.L., Lo S.H., Lin S., Butler J.A., Druker B.J.,  
RA Roberts T.M., An Q., Chen L.B.;  
RT "Presence of an SH2 domain in the actin-binding protein tensin."  
RL Science 252:712-715(1991).  
CC -!- FUNCTION: MAY BE INVOLVED IN CELL MIGRATION, CARTILAGE DEVELOPMENT  
CC AND IN LINKING SIGNAL TRANSDUCTION PATHWAYS TO THE CYTOSKELETON.  
CC BINDS TO ACTINS AND PHOSPHORYLATED PROTEINS IN SRC-TRANSFORMED  
CC CELLS. MAY BIND ACTIN WITH CAPPING AND BUNDLING PROPERTIES.  
CC -!- SUBCELLULAR LOCATION: LOCALIZES TO ADHERENS JUNCTIONS.  
CC -!- TISSUE SPECIFICITY: Heart, gizzard, lung and skeletal muscle.  
CC -!- PTM: Tyrosine phosphorylated.  
CC -!- SIMILARITY: Contains 1 tensin domain.  
CC -!- SIMILARITY: Contains 1 SH2 domain.  
CC  
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CC  
CC EMBL; M96625; AAA59053.1; -.  
CC EMBL; L06662; AAA73949.1; ALT\_INIT.  
CC EMBL; Z18529; CAA79215.1; ALT\_INIT.  
CC EMBL; M74165; AAA49087.1; -.  
CC EMBL; X66286; CAA46932.1; -.  
CC FIR; A54970; A54970.  
CC FIR; S27939; S27939.  
CC HSSP; P16277; 1BLK.  
CC InterPro; IPR008973; C2\_Calb.  
CC InterPro; IPR006020; PTB\_PID.  
CC InterPro; IPR000980; SH2.  
CC Pfam; PF00017; SH2; 1.  
CC ProDom; PD000093; SH2; 1.  
CC SMART; SM00462; PTB; 1.  
CC SMART; SM00252; SH2; 1.  
CC PROSITE; PS50001; SH2; 1.  
CC Actin-binding; Cytoskeleton; SH2 domain; Phosphorylation.  
XN DOMAIN 66 342  
FT DOMAIN 1472 1581  
FT SH2.  
FT CONFLICT 49 49 C -> R (IN REF. 2).  
FT CONFLICT 61 61 M -> T (IN REF. 2).  
FT CONFLICT 88 88 Q -> PR (IN REF. 3).  
FT CONFLICT 404 404 A -> T (IN REF. 2).  
FT CONFLICT 452 452 T -> A (IN REF. 2).  
FT CONFLICT 509 509 DV -> EL (IN REF. 2).  
FT CONFLICT 508 508 A -> P (IN REF. 2).  
FT CONFLICT 522 522 R -> A (IN REF. 2).  
FT CONFLICT 564 564 A -> T (IN REF. 2).  
FT CONFLICT 666 666 A -> T (IN REF. 2).

```
FT CONFLICT 875 875 P -> A (IN REF. 2).
FT CONFLICT 909 909 P -> T (IN REF. 2).
FT CONFLICT 1102 1113 MISSING (IN REF. 3).
FT CONFLICT 1240 1240 G -> A (IN REF. 2).
FT CONFLICT 1480 1480 E -> D (IN REF. 2).
FT CONFLICT 1711 1711 D -> E (IN REF. 2).
SQ SEQUENCE 1744 AA; 187214 MW; 5C3C8B6211935524 CRC64;

Query Match 56.5%; Score 35; DB 1; Length 1744;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 3 PGQELTKQ 10
Db 25 PGQSITKQ 32

RESULT 35
LEG4_CHICK
ID LEG4_CHICK STANDARD; PRT; 134 AA.
AC P07583;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Beta-galactoside-binding lectin (14 kDa lectin) (C-14).
OS Gallus gallus (Chicken).
OC Archosauria; Aves; Neognathae; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86130505; PubMed=3004444;
RA Ohnaya Y., Hirabayashi J., Oda Y., Ohno S., Kawasaki H., Suzuki K.,
RA Kasai K.-I.;
RT "Nucleotide sequence of chick 14K beta-galactoside-binding lectin
mRNA.";
RL Biochem. Biophys. Res. Commun. 134:51-56 (1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89033999; PubMed=3182759;
RA Ohnaya Y., Kasai K.-I.;
RT "Isolation and characterization of the chick 14K beta-galactoside-
binding lectin gene.";
RL J. Biochem. 104:173-177 (1988).
RN [3]
RP SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=87250364; PubMed=3597352;
RA Hirabayashi J., Kawasaki H., Suzuki K., Kasai K.-I.;
RT "Complete amino acid sequence of 14 kDa beta-galactoside-binding
lectin of chick embryo.";
RL J. Biochem. 101:775-783 (1987).
CC -!- FUNCTION: This protein binds beta-galactoside. Its physiological
function is not yet known. It may be involved in the regulation of
differentiation.
CC -!- SUBUNIT: Monomer (usually).
CC -!- TISSUE SPECIFICITY: Mainly in the intestine (adult), mainly in
the skin (embryo).
CC -!- SIMILARITY: Belongs to the galectin (galactin/s-lectin) family.
CC
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CC
CC EMBL; M11674; AAA48779.1; -.
DR EMBL; D00311; BAA00214.1; -.
DR EMBL; D00308; BAA00214.1; JOINED.
DR EMBL; D00309; BAA00214.1; JOINED.

DR EMBL; D00310; BAA00214.1; JOINED.
DR PIR; JX0042; LNCH14.
DR HSP; P11116; ISLT.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR001079; Galectin.
DR Pfam; PF00337; Gal-bind lectin; 1.
DR SMART; SM00276; GLECT; 1.
DR PROSITE; PS00309; GALAPTIN; 1.
KW Galectin; Lectin; Acetylation; Multigene family.
FT INIT MET 0 0
FT MOD RES 1 1 ACETYLATION.
FT BINDING 69 75 BETA-GALACTOSIDE (POTENTIAL).
SQ SEQUENCE 134 AA; 14932 MW; 0F60B30C9A26B053 CRC64;

Query Match 54.8%; Score 34; DB 1; Length 134;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 RPQELTKQ 11
Db 13 KPGQLTVKG 22

RESULT 36
IM23_SCHJA
ID IM23_SCHJA STANDARD; PRT; 218 AA.
AC P27591;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 23 kDa integral membrane protein (SU23).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92140457; PubMed=1779990;
RA Davern K.M., Wright M.D., Herrmann V.R., Mitchell G.F.;
RT "Further characterisation of the Schistosoma japonicum protein Sj23,
a target antigen of an immunodiagnostic monoclonal antibody.";
RL Mol. Biochem. Parasitol. 48:67-76 (1991).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC
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CC
CC EMBL; M63706; AAA29920.1; -.
DR PIR; A40181; A40181.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; transmembrane4; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
KW Glycoprotein; Antigen; Transmembrane.
FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 13 36 POTENTIAL.
FT DOMAIN 37 55 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 56 71 POTENTIAL.
FT DOMAIN 72 82 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 83 108 POTENTIAL.
FT DOMAIN 109 183 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 184 205 POTENTIAL.
FT DOMAIN 206 218 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 218 AA; 23728 MW; C2AE75DD5B60F23A CRC64;

Query Match 54.8%; Score 34; DB 1; Length 218;
Best Local Similarity 54.5%; Pred. No. 41;
```

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
 Db 161 CKEGQEVYVQG 171

RESULT 37  
 END3\_BACSU STANDARD; PRT; 219 AA.

AC P39788;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Probable endonuclease III (EC 4.2.99.18) (DNA- (apurinic or  
 DE apyrimidinic site) lyase).  
 GN NTH OR JOOB OR BSU22340.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=95219085; PubMed=7704260;  
 RT "Nucleotide sequence of the Bacillus subtilis dnaD gene.";  
 RL Microbiology 141:321-322(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168 / Mainzburg;  
 RX MEDLINE=96349105; PubMed=8760912;  
 RA Sorokin A.V., Azevedo V., Zumbstein E., Galleron N., Ehrlich S.D.,  
 RA Serror P.;  
 RT "Sequence analysis of the Bacillus subtilis chromosome region between  
 RT the serA and kgd loci cloned in a yeast artificial chromosome.";  
 RL Microbiology 142:2005-2016(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=98044033; PubMed=9384377;  
 RA Kunst P., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,  
 RA Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,  
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,  
 RA Etienne K.D., Errington J., Fabret C., Ferrari E., Foulger D.,  
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,  
 RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,  
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,  
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,  
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
 RA Parro V., Pohl T.M., Portetelle D., Portetelle S., Prescott A.M.,  
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,  
 RA Sato T., Scallan E., Schleich S., Schroeter R., Scotfone F.,  
 RA Sekiguchi J., Sekowska A., Serror S.J., Serror P., Shin B.S., Soldo B.,  
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
 RA Takeuchi M., Tanakoshi A., Tanaka T., Terstra P., Tognoni A.,  
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A.,  
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,  
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;  
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus  
 RT subtilis.";  
 RL Nature 390:249-256(1997).  
 CC -!- CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or  
 CC apyrimidinic site in DNA is broken by a beta-elimination reaction,

CC leaving a 3'-terminal unsaturated sugar and a product with a  
 CC terminal 5'-phosphate.  
 CC -!- COFACTOR: Binds a 4Fe-4S cluster which is not important for the  
 CC catalytic activity, but which is probably involved in the proper  
 CC positioning of the enzyme along the DNA strand (By similarity).  
 CC -!- SIMILARITY: Belongs to the nth/mutY family.  
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 CC  
 CC EMBL; U11289; AAA80005.1; -  
 CC EMBL; L47709; AAB38457.1; -  
 CC EMBL; Z91115; CAB14150.1; -  
 CC PIR; I40525; I40525.  
 CC HSSP; P20625; 2ABK.  
 CC Subtilist; BG10956; nth.  
 CC InterPro; IPR003265; Endo\_3c.  
 CC InterPro; IPR004035; EndoIII\_FCL.  
 CC InterPro; IPR004036; EndoIII\_HNH.  
 CC InterPro; IPR003651; Fes\_bind.  
 CC InterPro; IPR000445; Hnh.  
 CC InterPro; IPR003583; Hnh\_1.  
 CC InterPro; IPR005759; Nth.  
 CC Pfam; PF00730; Hnh-GPD; 1.  
 CC Pfam; PF06833; Hnh; 1.  
 CC SMART; SM00478; ENDO3c; 1.  
 CC SMART; SM00525; FES; 1.  
 CC SMART; SM00278; Hnh1; 1.  
 CC TIGRFAMs; TIGR01083; nth; 1.  
 CC PROSITE; PS00764; ENDONUCLEASE\_III\_1; 1.  
 CC PROSITE; PS01155; ENDONUCLEASE\_III\_2; 1.  
 CC KX Hydroxase; Nuclease; Iron-sulfur; Multifunctional enzyme; DNA repair;  
 KW Glycosidase; Lyase; Iron-sulfur; Complete proteome.  
 FT METAL 189 189 IRON-SULFUR (4FE-4S) (BY SIMILARITY).  
 FT METAL 196 196 IRON-SULFUR (4FE-4S) (BY SIMILARITY).  
 FT METAL 199 199 IRON-SULFUR (4FE-4S) (BY SIMILARITY).  
 FT METAL 205 205 IRON-SULFUR (4FE-4S) (BY SIMILARITY).  
 SQ SEQUENCE 219 AA; 25000 MW; C38C66DA7948BA40 CRC64;

Query Match 54.8%; Score 34; DB 1; Length 219;  
 Best Local Similarity 54.5%; Pred. No. 41;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
 Db 205 CREGQRDKKG 215

RESULT 38  
 AF01\_STRCO STANDARD; PRT; 225 AA.

ID AF01\_STRCO  
 AC Q04942; Q9AK20;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Transcriptional regulatory protein afsQ1.  
 DE AFSQ1 OR SCO4907 OR 2SCK8.33C.  
 GN Streptomyces coelicolor.  
 OS Bacteria; Actinobacteria; Actinomycetales;  
 OC Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ASP-52.  
 RC STRAIN=A3(2);  
 RX MEDLINE=93077438; PubMed=1339426;  
 RA Ishizuka H., Horinouchi S., Kiser H.M., Hopwood D.A., Beppu T.;  
 RT "A putative two-component regulatory system involved in secondary  
 RT metabolism in Streptomyces spp.";

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RL J. Bacteriol. 174:7595-7594 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21896410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Harris D.E., Quail M.A., Kieser H.,
RA Thomson N.R., James K.D., Harris D.E., Chandra G., Chen C.W., Collins M.,
RA Harper D., Bateman A., Brown S., Hdaigo J., Hornsby I., Howarth S.,
RA Cronin A., Fraser A., Goble A., Hdaigo J., Hornsby I., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitch E., Rajadrem M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147 (2002).
CC -1- FUNCTION: FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
CC -1- AFSQ1/AFS02 INVOLVED IN SECONDARY METABOLISM.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: Phosphorylated by afs02 (Potential).
CC -1- SIMILARITY: Contains 1 response regulatory domain.
CC
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CC
DR EMBL; D10654; BAA01502.1; -
DR EMBL; AL939121; CAC33072.1; -
DR PIR; A45270; A45270.
DR HSP; P08402; I800.
DR InterPro; IPR001789; Response_reg.
DR InterPro; IPR001867; Trans_reg_C.
DR Pfam; PF00072; response_reg; 1.
DR Pfam; PF00486; trans_reg_C; 1.
DR ProDom; PD000039; Response_reg; 1.
DR ProDom; PD000329; Trans_reg_C; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS50110; RESPONSE REGULATORY; 1.
KW Phosphorylation; Transcription regulation; DNA-binding;
KW Sensory transduction; Complete proteome.
FT DOMAIN 1 116 RESPONSE REGULATORY.
FT MOD_RES 52 52 PHOSPHORYLATION (BY SIMILARITY).
FT MUTAGEN 52 52 D->E: LOSS OF PROTEIN'S ABILITY TO
FT STIMULATE ANTIBIOTIC PRODUCTION AND
FT PIGMENTATION.
FT CONFLICT 11 11 D -> E (IN REF. 1).
SQ SEQUENCE 225 AA; 25106 MW; 2834669A9F3F1E3E CRC64;
Query Match 54.8%; Score 34; DB 1; Length 225;
Best Local Similarity 66.7%; Pred. No. 43;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 RFGQLTKQ 10
DB 164 RFGQALSQ 172
RESULT 39
TR18 HUMAN
ID TR18 HUMAN STANDARD; PRT; 241 AA.
AC Q9Y5U5; Q95851; Q9NY09;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 18 precursor
DE (Glucocorticoid-induced TNFR-related protein) (Activation-inducible
DE TNFR family receptor).
GN TNFRSF18 OR GITR OR AITR.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH TRAF1; TRAF2 AND
RP TRAF3.
RC TISSUE=Bone marrow;
RX MEDLINE=99175482; PubMed=10074428;
RA Gurney A.L., Marschers S.A., Huang R.M., Pitti R.M., Mark D.T.,
RA Baldwin D.T., Gray A.M., Dowd A.D., Brush A.D., Heidens A.D.,
RA Schow A.D., Goddard A.D., Wood W.I., Baker K.P., Godowski P.J.,
RA Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family
RT and its receptor, a human ortholog of mouse GITR.";
RL Curr. Biol. 9:215-218 (1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=T-cell;
RX MEDLINE=99156876; PubMed=10037686;
RA Kwon B., Yu K.-Y., Ni J., Yu G.-L., Jang I.-K., Kim Y.-J., Xing L.,
RA Liu D., Wang S.-X., Kwon B.S.;
RT "Identification of a novel activation-inducible protein of the tumor
RT necrosis factor receptor superfamily and its ligand.";
RL J. Biol. Chem. 274:6056-6061 (1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Thymus;
RX MEDLINE=20292073; PubMed=10836847;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Brunetti L., Magliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GITR.";
RL Cell Death Differ. 7:408-410 (2000).
CC -1- FUNCTION: Receptor for TNFSF18. Seems to be involved in
CC interactions between activated T lymphocytes and endothelial cells
CC and in the regulation of T cell receptor-mediated cell death.
CC Mediated NF-kappa-B activation via the TRAF2/NIK pathway.
CC -1- SUBUNIT: Binds to TRAF1, TRAF2, and TRAF3, but not TRAF5 and
CC TRAF6.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
CC Secreted (isoform 2).
CC -1- ALTERNATIVE PRODUCTS.
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9Y5U5-1; Sequence=Displayed;
CC Name=2; Synonyms=GITR-D;
CC IsoId=Q9Y5U5-2; Sequence=VSP_006508;
CC -1- TISSUE SPECIFICITY: Expressed in lymph node, peripheral blood
CC leukocytes and weakly in spleen.
CC -1- INDUCTION: Upregulated in peripheral mononuclear cells after
CC antigen stimulation/lymphocyte activation.
CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AF125304; AAD22635.1; -
DR EMBL; AF117297; AAD19694.1; -
DR EMBL; AF241229; AAF63506.1; -
DR Genew; HGNC:11914; TNFRSF18.
DR MIM; 603905; -
DR GO; GO:0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.
DR GO; GO:0006916; P:anti-apoptosis; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR001368; TNFR_c6.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
DR

```

Search completed: May 5, 2004, 14:38:41  
Job time : 1.86644 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:34:21 ; Search time 3.76712 Seconds  
(without alignments)  
921.313 Million cell updates/sec

Title: US-10-067-122B-2\_COPY\_105\_115  
Perfect score: 62  
Sequence: 1 CRPGQELTKQG 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL 25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	211	11	Q8R037
2	43	69.4	880	4	Q8NAU9
3	43	69.4	993	4	Q8IX30
4	41	66.1	147	4	Q8IYV5
5	40	64.5	185	11	Q8B3S6
6	40	64.5	297	11	Q8BX35
7	40	64.5	297	11	Q8BN50
8	40	64.5	318	4	Q8IZA6
9	40	64.5	379	16	Q87QQ8
10	40	64.5	443	10	Q944J9
11	40	64.5	459	10	Q9SF11
12	40	64.5	706	11	Q8CFG9
13	40	64.5	707	11	Q99KI6
14	40	64.5	707	11	Q9ET60
15	40	64.5	707	11	Q8CG16
16	40	64.5	2809	4	Q96JP8

17	40	64.5	2809	4	Q86SJ5	Q86sj5 homo sapien
18	39	62.9	250	11	Q8C4K3	Q8c4k3 mus musculus
19	38	61.3	213	16	Q88UD7	Q88jd7 pseudomonas
20	38	61.3	249	12	Q82036	Q82036 hirame rhab
21	38	61.3	307	4	Q9H9A3	Q9h9a3 homo sapien
22	38	61.3	391	12	Q88449	Q88449 infectious
23	38	61.3	391	12	Q82680	Q82680 infectious
24	38	61.3	391	12	Q82679	Q82679 infectious
25	38	61.3	392	12	Q9QL89	Q9ql89 hirame rhab
26	38	61.3	417	4	Q9UFH0	Q9ufh0 homo sapien
27	38	61.3	594	4	Q96K47	Q96k47 homo sapien
28	38	61.3	654	16	Q7UYT4	Q7uyt4 rhodospirell
29	38	61.3	753	4	Q81WF8	Q81wf8 homo sapien
30	38	61.3	780	10	Q94H84	Q94h84 oryza sativ
31	38	61.3	793	4	Q7Z3N3	Q7z3n3 homo sapien
32	38	61.3	978	5	Q9U5P6	Q9u5p6 haemonchus
33	38	61.3	997	11	Q9JUS0	Q9jjs0 mus musculus
34	38	61.3	999	4	Q9NQ36	Q9nq36 homo sapien
35	38	61.3	1207	10	Q9LPK1	Q9lpx1 arabidopsis
36	38	61.3	1334	10	Q9C7Y1	Q9c7y1 arabidopsis
37	38	61.3	1334	10	Q9FH39	Q9fh39 arabidopsis
38	38	61.3	1335	10	Q8H3Z6	Q8h3z6 oryza sativ
39	37	59.7	110	5	Q24406	Q24406 drosophila
40	37	59.7	110	5	Q24402	Q24402 drosophila
41	37	59.7	144	5	Q9VJR1	Q9vjr1 drosophila
42	37	59.7	146	5	Q9NKA7	Q9nka7 drosophila
43	37	59.7	160	4	Q8NB54	Q8nb54 homo sapien
44	37	59.7	196	11	Q8VC17	Q8vc17 mus musculus
45	37	59.7	214	11	Q812G3	Q812g3 mus musculus

#### ALIGNMENTS

RESULT 1

Q8R037 PRELIMINARY; PRT; 211 AA.  
AC Q8R037;  
DT 01-JUN-2002 (TRENBLrel. 21, Created)  
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE Similar to tumor necrosis factor receptor superfamily, member 9.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=uterus;  
RA Strausberg R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC028507; AAH28507.1; -.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 1.  
DR SMART; SM00208; TNFR; 2.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
KW Receptor.  
SQ SEQUENCE 211 AA; 22452 MW; 1EECA84EA32A8D50 CRC64;

Query Match 100.0%; Score 62; DB 11; Length 211;

Best Local Similarity 100.0%; Pred.No. 0.001; Mismatches 0; Gaps 0;

Matches 11; Conservative 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11

Db 105 CRPGQELTKQG 115

RESULT 2

Q8NAU9

ID Q8NAU9 PRELIMINARY; PRT; 880 AA.  
 AC Q8NAU9;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein FLJ34743.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,  
 RA Furiya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,  
 RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,  
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,  
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,  
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,  
 RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,  
 RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.,  
 RT "NEBO human cDNA sequencing project";  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 CC !- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
 DR EMBL; AK092062; BAC03798.1; -;  
 DR Genew; HGNC:13655; CEGF3.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005509; P:calcium ion binding; IEA.  
 DR GO; GO:0004888; P:transmembrane receptor activity; IEA.  
 DR GO; GO:0007596; P:blood coagulation; IEA.  
 DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
 DR InterPro; IPR000859; CUB.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR009030; Grow\_fac\_recep.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR001491; Thrbomoduln.  
 DR Pfam; PF00431; CUB; 1.  
 DR Pfam; PF00008; EGF; 6.  
 DR PRINTS; PRO0907; THRBOMODULN.  
 DR SMART; SM00042; CUB; 1.  
 DR SMART; SM00181; EGF; 8.  
 DR SMART; SM00179; EGF\_Ca; 5.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
 DR PROSITE; PS01180; CUB; 1.  
 DR PROSITE; PS01186; EGF; 2; 5.  
 DR PROSITE; PS01187; EGF\_Ca; 3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 880 AA; 97239 MW; F0BDE6E85266FD60 CRC64;

Query Match 69.4%; Score 43; DB 4; Length 880;  
 Best Local Similarity 88.9%; Pred. No. 21;  
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;  
 QY 1 CRPGQELTK 9  
 DB 55 CRPGFELTK 63  
 |||||  
 |||||

RESULT 3  
 Q8IX30 PRELIMINARY; PRT; 993 AA.  
 ID Q8IX30;  
 AC Q8IX30;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE CUB and EGF containing protein.  
 GN CEGF3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Pfarr N., Bahr A., Cichutek A., Loebbert R., Zabel B.U., Schmidt E.R.,  
 RA Haneln T., Winterpacht A.;  
 RT "Novel human gene family (CEGF) encoding mosaic proteins with EGF-  
 RT like, STR2R and a CUB module: cloning and expression analysis.";  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF454494; AAN76808.1; -;  
 DR GO; GO:0005509; P:calcium ion binding; IEA.  
 DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
 DR InterPro; IPR000859; CUB.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR009030; Grow\_fac\_recep.  
 DR InterPro; IPR006210; IEGF.  
 DR Pfam; PF00431; CUB; 1.  
 DR Pfam; PF00008; EGF; 9.  
 DR SMART; SM00042; CUB; 1.  
 DR SMART; SM00181; EGF; 10.  
 DR SMART; SM00179; EGF\_Ca; 7.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 6.  
 DR PROSITE; PS01180; CUB; 1.  
 DR PROSITE; PS01186; EGF; 2; 7.  
 DR PROSITE; PS01187; EGF\_Ca; 6.  
 SQ SEQUENCE 993 AA; 109282 MW; 19BBE0E5627BEAF4 CRC64;

Query Match 69.4%; Score 43; DB 4; Length 993;  
 Best Local Similarity 88.9%; Pred. No. 23;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CRPGQELTK 9  
 DB 184 CRPGFELTK 192  
 |||||  
 |||||

RESULT 4  
 Q8IYV5 PRELIMINARY; PRT; 147 AA.  
 ID Q8IYV5;  
 AC Q8IYV5;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skin;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC033292; AAH33292.1; -;  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004896; P:hematopoietin/interferon-class (D200-domain...); IEA.  
 DR InterPro; IPR000282; Cytok\_receptor\_2.  
 DR InterPro; IPR008957; FN\_III-like.  
 KW Hypothetical protein.  
 SQ SEQUENCE 147 AA; 16945 MW; 71BAF49274618999 CRC64;

Query Match 66.1%; Score 41; DB 4; Length 147;  
 Best Local Similarity 70.0%; Pred. No. 7.5;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 RFGQELTKG 11  
 DB 93 RFGMEITKG 102  
 |||||  
 |||||

RESULT 5  
 Q8BJ56 PRELIMINARY; PRT; 185 AA.  
 ID Q8BJ56;  
 AC Q8BJ56;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

01-OCT-2003 (Tremblrel. 25, Last annotation update)  
Similar to X-linked ectodysplasin-A receptor.  
Mus musculus (Mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=C57BL/6J; TISSUE=Aorta, and Vein;  
MEDLINE=22354683; PubMed=12466851;  
The FANTOM Consortium,  
the RIKEN Genome Exploration Research Group Phase I & II Team;  
"Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs."  
Nature 420:563-573(2002).  
EMBL; AK080072; BAC37822.1; -.  
MGI; MGI:2442860; Xedar.  
GO; GO:0004872; F:receptor activity; IEA.  
InterPro; IPR001368; TNFR\_c6.  
Pfam; PF00020; TNFR\_c6; 2.  
SMART; SM00208; TNFR; 2.  
PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
PROSITE; PS00050; TNFR\_NGFR\_2; 1.  
SEQUENCE 185 AA; 20532 MW; 7335CCAC83C829C4 CRC64;  
Query Match 64.5%; Score 40; DB 11; Length 185;  
Best Local Similarity 77.8%; Pred. No. 15;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CRPGQELTK 9  
| | | | | | | | | |  
Db 21 CGPGQELSK 29  
RESULT 6  
Q8BX35 Q8BX35 PRELIMINARY; PRT; 297 AA.  
AC Q8BX35;  
DT 01-MAR-2003 (Tremblrel. 23, Created)  
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Similar to X-linked ectodysplasin-A receptor.  
GN XEDAR OR 9430060M22RIK.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OC NCBI\_TaxID=10090;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=C57BL/6J;  
MEDLINE=22354683; PubMed=12466851;  
The FANTOM Consortium,  
the RIKEN Genome Exploration Research Group Phase I & II Team;  
"Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs."  
Nature 420:563-573(2002).  
EMBL; AK049134; BAC33562.1; -.  
MGI; MGI:2442860; Xedar.  
GO; GO:0004872; F:receptor activity; IEA.  
InterPro; IPR001368; TNFR\_c6.  
Pfam; PF00020; TNFR\_c6; 2.  
SMART; SM00208; TNFR; 2.  
PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
PROSITE; PS00050; TNFR\_NGFR\_2; 1.  
SEQUENCE 297 AA; 33066 MW; 46FEFD5C1D739BE CRC64;  
Query Match 64.5%; Score 40; DB 11; Length 297;  
Best Local Similarity 77.8%; Pred. No. 25;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CRPGQELTK 9  
| | | | | | | | | |

Db 21 CGPGQELSK 29  
RESULT 7  
Q8BM50 Q8BM50 PRELIMINARY; PRT; 297 AA.  
AC Q8BM50;  
DT 01-MAR-2003 (Tremblrel. 23, Created)  
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Similar to X-linked ectodysplasin-A receptor.  
GN XEDAR OR 9430060M22RIK.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OC NCBI\_TaxID=10090;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=C57BL/6J; TISSUE=Embryo;  
MEDLINE=22354683; PubMed=12466851;  
The FANTOM Consortium,  
the RIKEN Genome Exploration Research Group Phase I & II Team;  
"Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs."  
Nature 420:563-573(2002).  
EMBL; AK034909; BAC28879.1; -.  
MGI; MGI:2442860; Xedar.  
GO; GO:0004872; F:receptor activity; IEA.  
InterPro; IPR001368; TNFR\_c6.  
Pfam; PF00020; TNFR\_c6; 2.  
SMART; SM00208; TNFR; 2.  
PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
PROSITE; PS00050; TNFR\_NGFR\_2; 1.  
SEQUENCE 297 AA; 33038 MW; D5F2CD188765AD65 CRC64;  
Query Match 64.5%; Score 40; DB 11; Length 297;  
Best Local Similarity 77.8%; Pred. No. 25;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CRPGQELTK 9  
| | | | | | | | | |  
Db 21 CGPGQELSK 29  
RESULT 8  
Q8IZA6 Q8IZA6 PRELIMINARY; PRT; 318 AA.  
AC Q8IZA6;  
DT 01-MAR-2003 (Tremblrel. 23, Created)  
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE X-linked ectodermal dysplasia receptor long isoform.  
GN XEDAR.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=22323114; PubMed=12270937;  
Sinha S.K., Zachariah S., Quinones H.I., Shindo M., Chaudhary P.M.;  
"Role of TRAF3 and -6 in the activation of the NF-kappa B and JNK  
Pathways by X-linked Ectodermal Dysplasia Receptor.";  
J. Biol. Chem. 277:44953-44961(2002).  
EMBL; AY152724; AAN73210.1; -.  
GO; GO:0004872; F:receptor activity; IEA.  
InterPro; IPR001368; TNFR\_c6.  
Pfam; PF00020; TNFR\_c6; 2.  
SMART; SM00208; TNFR; 2.  
PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
Receptor.  
SEQUENCE 318 AA; 34992 MW; A4C8AED32F346A3E CRC64;

Query Match 64.5%; Score 40; DB 4; Length 318;  
 Best Local Similarity 77.8%; Pred. No. 27;  
 Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 CRPGQELTK 9  
 | | | | | | | |  
 Db 21 CGPGQELSK 29

RESULT 9  
 Q87Q08 PRELIMINARY; PRT; 379 AA.  
 ID Q87Q08;  
 AC Q87Q08;  
 DT 01-JUN-2003 (TREMELrel. 24, Created)  
 DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE Putative transmembrane protein affecting septum formation and cell  
 DE membrane permeability.  
 GN VP1091.  
 OS Vibrio parahaemolyticus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=670;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RIMD 2210633 / Serotype O3:K6;  
 RX MEDLINE=22508454; PubMed=12620739;  
 RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,  
 RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,  
 RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;  
 RT "Genome sequence of *Vibrio parahaemolyticus*: a pathogenic mechanism  
 RT distinct from that of *V. cholerae*.";  
 RL Lancet 361:743-749 (2003).  
 DR EMBL; AF005076; BACS9354.1; -  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0008565; P:protein transporter activity; IEA.  
 DR GO; GO:0009306; P:protein secretion; IEA.  
 DR InterPro; IPR006143; Hyd.  
 DR InterPro; IPR000437; Prok\_lipoprot\_S.  
 DR Pfam; PF00529; Hyd; 1.  
 DR PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.  
 KW Transmembrane; Complete proteome.  
 SQ SEQUENCE 379 AA; 40389 MW; 97938BB9E2268CDB CRC64;

Query Match 64.5%; Score 40; DB 16; Length 379;  
 Best Local Similarity 63.6%; Pred. No. 32;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPGQELTKQ 11  
 | | | | | | | |  
 Db 20 CQPSQEGTEQ 30

RESULT 10  
 Q944J9 PRELIMINARY; PRT; 443 AA.  
 ID Q944J9;  
 AC Q944J9;  
 DT 01-DEC-2001 (TREMELrel. 19, Created)  
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
 DE AT3G11880/F26K24.17.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,  
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,  
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,  
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,

RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,  
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,  
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,  
 RA Ecker J.R.;  
 RT "Arabidopsis cDNA clones.";  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AF428353; AAL16283.1; -  
 SQ SEQUENCE 443 AA; 49596 MW; 6FFB2BB1673607C1 CRC64;

Query Match 64.5%; Score 40; DB 10; Length 443;  
 Best Local Similarity 70.0%; Pred. No. 38;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQ 10  
 | | | | | | | |  
 Db 286 CPGGSELMKQ 295

RESULT 11  
 Q9SF11 PRELIMINARY; PRT; 459 AA.  
 ID Q9SF11;  
 AC Q9SF11;  
 DT 01-MAY-2000 (TREMELrel. 13, Created)  
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
 DE F26K24.17 protein.  
 GN F26K24.17.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,  
 RA Rensing C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,  
 RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;  
 RT "Arabidopsis thaliana chromosome III BAC F26K24 genomic sequence.";  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AC016795; AAF23204.1; -  
 SQ SEQUENCE 459 AA; 51414 MW; CE3994D766025B8F9 CRC64;

Query Match 64.5%; Score 40; DB 10; Length 459;  
 Best Local Similarity 70.0%; Pred. No. 39;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQ 10  
 | | | | | | | |  
 Db 302 CPGGSELMKQ 311

RESULT 12  
 Q8CFG9 PRELIMINARY; PRT; 706 AA.  
 ID Q8CFG9;  
 AC Q8CFG9;  
 DT 01-MAR-2003 (TREMELrel. 23, Created)  
 DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE Complement component C1RB.  
 GN C1R OR C1RB.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Accessory reproductive organs;  
 RA Garner G., Circolo A., Xu Y., Volanakis J.E.;  
 RT "The murine C1r/C1s gene cluster.";  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AP459018; AAO15557.1; -  
 MGD; MGI:1355313; C1r.

DR GO:0005509; F:calcium ion binding; IEA.  
DR GO:0004263; F:chymotrypsin activity; IEA.  
DR GO:0004295; F:trypsin activity; IEA.  
DR GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
DR Pfam; PF00431; CUB; 2.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00084; sushi; 2.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00032; CCP; 2.  
DR SMART; SM00042; CUB; 2.  
DR SMART; SM00179; EGF\_Ca; 1.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS01180; CUB; 2.  
DR PROSITE; PS01186; EGF; 2.  
DR PROSITE; PS01187; EGF\_Ca; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW EGF-like domain; Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 706 AA; 79936 MW; 092684922F41A64F CRC64;

Query Match 64.5%; Score 40; DB 11; Length 706;  
Best Local Similarity 63.6%; Pred. No. 62;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRPQELTKQG 11  
DB 175 CHPGYELQKDG 185

RESULT 13  
ID Q99KI6 PRELIMINARY; PRT; 707 AA.  
AC Q99KI6;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Complement component 1, r subcomponent.  
GN Clr.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
DR EMBL; BC004637; AA04637.1; -.  
DR HSP; P00736; IAPQ.  
DR MEROPS; S01.192; -.  
DR MGD; MGI:1355313; Clr.  
DR GO:0005509; F:calcium ion binding; IEA.  
DR GO:0004263; F:chymotrypsin activity; IEA.  
DR GO:0008233; F:peptidase activity; IEA.  
DR GO:0004295; F:trypsin activity; IEA.  
DR GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR00859; CUB.  
DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR Pfam; PF00431; CUB; 2.  
DR Pfam; PF00084; sushi; 2.

DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
DR Pfam; PF00431; CUB; 2.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00084; sushi; 2.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00032; CCP; 2.  
DR SMART; SM00042; CUB; 2.  
DR SMART; SM00179; EGF\_Ca; 1.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS01180; CUB; 2.  
DR PROSITE; PS01186; EGF; 2.  
DR PROSITE; PS01187; EGF\_Ca; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW EGF-like domain; Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 707 AA; 80096 MW; BF0D3F47201DB8B1 CRC64;

Query Match 64.5%; Score 40; DB 11; Length 707;  
Best Local Similarity 63.6%; Pred. No. 62;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRPQELTKQG 11  
DB 175 CHPGYELQKDG 185

RESULT 14  
ID Q9ET60 PRELIMINARY; PRT; 707 AA.  
AC Q9ET60;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Serine protease.  
GN Clr.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strain-C57BL/6;  
RA Byun S.-J., Hyun J.H., Hwang H.-Y., Ryoo Z.-Y., Kim T.-Y.;  
RT "Cloning and Sequencing of a cDNA Encoding a Serine Protease Homologous to Human Complement C1r Precursor from an Allografted Mouse Skin and Its Expression in Escherichia coli."  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
DR EMBL; AF148216; AAG01898.1; -.  
DR HSP; P00736; IAPQ.  
DR MEROPS; S01.192; -.  
DR MGD; MGI:1355313; Clr.  
DR GO:0005509; F:calcium ion binding; IEA.  
DR GO:0004263; F:chymotrypsin activity; IEA.  
DR GO:0008233; F:peptidase activity; IEA.  
DR GO:0004295; F:trypsin activity; IEA.  
DR GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR00859; CUB.  
DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR Pfam; PF00431; CUB; 2.  
DR Pfam; PF00084; sushi; 2.

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DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00020; trypt_spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 707 AA; 80142 MW; CC90F1163A52D824 CRC64;

Query Match 64.5%; Score 40; DB 11; Length 707;
Best Local Similarity 63.6%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
DB 175 CHPGYELQKDG 185

RESULT 15
Q8CG16 PRELIMINARY; PRT; 707 AA.
ID Q8CG16
AC Q8CG16;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Complement component C1RA.
GN C1RA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-129/Svj;
RA Garner G., Circolo A., Xu Y., Volanakis J.E.;
RT "The murine C1r/C1s gene cluster.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF459011; AAO15553.1; -.
DR EMBL; AF459008; AAO15553.1; JOINED.
DR EMBL; AF459009; AAO15553.1; JOINED.
DR EMBL; AF459010; AAO15553.1; JOINED.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; sushi; 2.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00020; trypt_spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01186; EGF_2; 1.

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DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR SEQUENCE 707 AA; 80073 MW; 29DAAEB3C047D8E8 CRC64;

Query Match 64.5%; Score 40; DB 11; Length 707;
Best Local Similarity 63.6%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
DB 175 CHPGYELQKDG 185

RESULT 16
Q96JP8 PRELIMINARY; PRT; 2809 AA.
ID Q96JP8
AC Q96JP8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibrillin3.
GN KIAA1776.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21245130; PubMed=11347906;
RA Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XX.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 8:95-95(2001).
DR EMBL; AB053450; BAB47408.1; -.
DR Genew; HGNC:18794; FBN3.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002212; Fibril-assoc.
DR Pfam; PF00008; EGF; 42.
DR Pfam; PF00683; TB; 9.
DR SMART; SM00179; EGF_CA; 41.
DR PROSITE; PS00010; ASX_HYDROXYL; 41.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 36.
DR PROSITE; PS01187; EGF_CA; 40.
DR EGF-like domain.
KW EGF-like domain.
SQ SEQUENCE 2809 AA; 300323 MW; 20C04CC006C0161F CRC64;

Query Match 64.5%; Score 40; DB 4; Length 2809;
Best Local Similarity 63.6%; Pred. No. 2.7e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
DB 1098 CPPGHLETKAG 1108

RESULT 17
Q86SJ5 PRELIMINARY; PRT; 2809 AA.
ID Q86SJ5
AC Q86SJ5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibrillin-3 short form precursor transcript variant 1 (Fibrillin-3
DE short form precursor transcript variant 2) (Fibrillin-3 short form
DE precursor transcript variant 3).
GN FBN3.

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OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Corson G.M., Charbonneau N.L., Keene D.R., Sakai L.Y.;  
RT "A Third Fibrillin Adds Diversity to Extracellular Microfibrils";  
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY165863; AAC18145.1; -  
DR EMBL; AY165864; AAC18146.1; -  
DR EMBL; AY165865; AAC18147.1; -  
DR GO; GO:0005509; Focalium ion binding; IEA.  
DR InterPro; IPR000152; Asx hydroxylase.  
DR InterPro; IPR001881; EGF CA.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR002212; Fibril-associ.  
DR InterPro; IPR006210; IEGF.  
DR Pfam; PF00008; EGF; 45.  
DR Pfam; PF00683; TB; 9.  
DR SMART; SM00181; EGF; 46.  
DR SMART; SM00179; EGF CA; 43.  
DR PROSITE; PS00010; ASX HYDROXYL; 41.  
DR PROSITE; PS00022; EGF 1; 2.  
DR PROSITE; PS01186; EGF 2; 36.  
DR PROSITE; PS01187; EGF CA; 40.  
KW Signal.  
FT SIGNAL 1 29 POTENTIAL.  
FT CHAIN 48 2689 FIBRILLIN-3 SHORT FORM.  
SQ SEQUENCE 2809 AA; 300367 MW; 064F6FFB8E239473 CRC64;  
  
Query Match 64.58; Score 40; DB 4; Length 2809;  
Best Local Similarity 63.64; Pred. No. 2.7e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 CRPGQELTKQG 11  
DB 1098 CPFGHELTAKG 1108  
||| ||| |||  
  
RESULT 18  
Q8C4K3 PRELIMINARY; PRT; 250 AA.  
AC Q8C4K3  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Tumor necrosis factor receptor superfamily.  
GN TNFRSF18.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=C57BL/6J; TISSUE=Head;  
RC MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium.  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs";  
RL Nature 420:563-573(2002).  
DR EMBL; AK081878; BAC38357.1; -  
DR MGD; MGI:894675; Tnf18.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR001368; TNFR\_c6.  
DR SMART; SM00208; TNFR; 2.  
SQ SEQUENCE 250 AA; 27814 MW; 6963E94F414C16B4 CRC64;  
  
Query Match 62.9%; Score 39; DB 11; Length 250;  
Best Local Similarity 54.5%; Pred. No. 32;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
DB 82 CQPGQVESQ 92  
||| ||| |||  
  
RESULT 19  
Q88JD7 PRELIMINARY; PRT; 213 AA.  
AC Q88JD7  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Conserved domain protein.  
GN PP212.  
OS Pseudomonas putida (strain KT2440).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=160488;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=24423060; PubMed=12534463;  
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,  
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,  
RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,  
RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,  
RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,  
RA Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,  
RA Lauber J., Stjepandic D., Hohnselt J., Straetz M., Haim S.,  
RA Kiewitz C., Eissen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,  
RA Fraser C.M.;  
RT "Complete genome sequence and comparative analysis of the  
RT metabolically versatile Pseudomonas putida KT2440";  
RL Environ. Microbiol. 4:799-808(2002).  
DR EMBL; AE016784; AAN68320.1; -  
DR TIGR; PF2712; -  
DR InterPro; IPR001440; TPR.  
DR InterPro; IPR008941; TPR-like.  
KW Complete proteome.  
SQ SEQUENCE 213 AA; 23480 MW; 6E89CB3C04EBC420 CRC64;  
  
Query Match 61.3%; Score 38; DB 16; Length 213;  
Best Local Similarity 70.0%; Pred. No. 42;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 CRPGQELTKQG 11  
DB 187 RRGRELADQG 196  
||| ||| |||  
  
RESULT 20  
Q82036 PRELIMINARY; PRT; 249 AA.  
AC Q82036  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Nucleocapsid protein.  
GN N.  
OS Hirame rhabdovirus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Rhabdoviridae; Novirhabdovirus.  
OX NCBI\_TaxID=38142;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Nishizawa T.;  
RA STRAIN=8401-H;  
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; D45422; BAA08261.1; -  
DR GO; GO:0015013; Civil nuclear nucleocapsid; IEA.  
DR InterPro; IPR004902; Rhabdo\_ncap\_2.  
DR Pfam; PF03216; Rhabdo\_ncap\_2; 1.  
SQ SEQUENCE 249 AA; 26936 MW; 62FF2BFASD47DB89 CRC64;

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Query Match          61.3%; Score 38; DB 12; Length 249;
Best Local Similarity 87.5%; Pred. No. 50;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RPOQELTK 9
DB 39 RPOQKLTK 46

RESULT 21
Q9H9A3
ID Q9H9A3 PRELIMINARY; PRT; 307 AA.
AC Q9H9A3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ12892.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayaashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y., Oshima A.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK022954; BAB14329.1;
KW Hypothetical protein.
SQ SEQUENCE 307 AA; 6833080C80898933 CRC64;

Query Match          61.3%; Score 38; DB 4; Length 307;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
DB 15 CRPGNNLTK 23

RESULT 22
Q08449
ID Q08449 PRELIMINARY; PRT; 391 AA.
AC Q08449;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Nucleocapsid protein (Nucleoprotein).
GN N.
OS Infectious hematopoietic necrosis virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Novirhabdovirus.
OX NCBI_TaxID=11290;
RN [1]
RP SEQUENCE FROM N.A.
RA Schuetze H., Enzmann P.J., Kuchling R., Mundt E., Niemann H.,
RA Mettenleiter T.C.;
RL J. Gen. Virol. 14:2519-2527(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K;
RA Schuetze H.;
RL Submitted (JUL-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-5 FROM N.A.
RC STRAIN=K;
RX MEDLINE=89073771; PubMed=3201758;
RA Gilmore R.D., Leong J.C.;
RT "The nucleocapsid gene of infectious hematopoietic necrosis virus, a
RT fish rhabdovirus.";

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Virology 167:644-648(1988).
CC -1- PTM: PHOSPHORYLATED (BY SIMILARITY).
CC -1- SIMILARITY: TO VHSV NUCLEOCAPSID PROTEIN.
DR EMBL; X73872; CAAG2071.1;
DR EMBL; X89213; CAAG1495.1;
DR GO; GO:0019013; C:Viral nucleocapsid; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR001179; FKBP PPIase.
DR InterPro; IPR004902; Rhabdo ncaps_2.
DR Pfam; PF03216; Rhabdo ncaps_2; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
KW Nucleocapsid; Phosphorylation.
SQ SEQUENCE 391 AA; 42309 MW; 88FF0C5E2B03D32B CRC64;

Query Match          61.3%; Score 38; DB 12; Length 391;
Best Local Similarity 87.5%; Pred. No. 80;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RPOQELTK 9
DB 183 RPOQKLTK 190

RESULT 23
Q82680
ID Q82680 PRELIMINARY; PRT; 391 AA.
AC Q82680;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Nucleocapsid protein.
GN N GENE.
OS Infectious hematopoietic necrosis virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Novirhabdovirus.
OX NCBI_TaxID=11290;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WRAC;
RX MEDLINE=96118173; PubMed=8578857;
RA Morzunov S.P., Winton J.R., Nichol S.T.;
RT "The complete genome structure and phylogenetic relationship of
RT infectious hematopoietic necrosis virus.";
RL Virus Res. 38:175-192(1995).
DR EMBL; L40883; AAC42150.1;
DR GO; GO:0019013; C:Viral nucleocapsid; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR001179; FKBP PPIase.
DR InterPro; IPR004902; Rhabdo ncaps_2.
DR Pfam; PF03216; Rhabdo ncaps_2; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
SQ SEQUENCE 391 AA; 42208 MW; 959C930C080E55D8 CRC64;

Query Match          61.3%; Score 38; DB 12; Length 391;
Best Local Similarity 87.5%; Pred. No. 80;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RPOQELTK 9
DB 183 RPOQKLTK 190

RESULT 24
Q82679
ID Q82679 PRELIMINARY; PRT; 391 AA.
AC Q82679;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Nucleoprotein.
GN N.
OS Infectious hematopoietic necrosis virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

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DR	EMBL; ALJ122079; CAB59254.1; -.
DR	NCBI_TaxID=11290;
RN	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=Round Butte 1;
RC	Emmenegger E.J., Kurath G.;
RL	Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RA	EMBL; U50402; AAA97895.1; -.
DR	GO; GO:0019013; C:Viral nucleocapsid; IEA.
DR	InterPro; IPR004902; Rhabdo_ncap_2.
DR	Pfam; PF03216; Rhabdo_ncap_2; 1.
SQ	SEQUENCE 391 AA; 42073 MW; 7F9F11640AA7AA6D CRC64;
Query Match	
Best Local Similarity 61.3%; Score 38; DB 12; Length 391;	
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	2 RPQGKLTk 9
Db	183 RPQGKLTk 190
RESULT 25	
ID	Q9QL89 PRELIMINARY; PRT; 392 AA.
AC	Q9QL89;
DT	01-MAY-2000 (TREMBlrel. 13, Created)
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE	Nucleocapsid protein.
OS	Hirame rhabdovirus.
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC	Rhabdoviridae; Novirhabdovirus.
NCBI_TaxID=38142;	
RN	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=CA 9703;
RC	Oh H.K., Choi T.J.;
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RA	EMBL; AF104985; AAF14116.1; -.
DR	GO; GO:0019013; C:Viral nucleocapsid; IEA.
DR	InterPro; IPR004902; Rhabdo_ncap_2.
DR	Pfam; PF03216; Rhabdo_ncap_2; 1.
SQ	SEQUENCE 392 AA; 42465 MW; C5A282238FC7A638 CRC64;
Query Match	
Best Local Similarity 61.3%; Score 38; DB 12; Length 392;	
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	2 RPQGKLTk 9
Db	182 RPQGKLTk 189
RESULT 26	
ID	Q9UFH0 PRELIMINARY; PRT; 417 AA.
AC	Q9UFH0;
DT	01-MAY-2000 (TREMBlrel. 13, Created)
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE	Hypothetical protein (fragment).
GN	DXFPZP434LI050.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;	
RN	[1]
RN	SEQUENCE FROM N.A.
RC	TISSUE=Testis;
RC	Tissuetestis;
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RA	PoustaKa A., Klein M., Mwes H.W., Gassenhuber J., Wiemann S.;

DR	EMBL; ALJ122079; CAB59254.1; -.
DR	NCBI_TaxID=11290;
RN	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=Round Butte 1;
RC	Emmenegger E.J., Kurath G.;
RL	Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RA	EMBL; U50402; AAA97895.1; -.
DR	GO; GO:0019013; C:Viral nucleocapsid; IEA.
DR	InterPro; IPR004902; Rhabdo_ncap_2.
DR	Pfam; PF03216; Rhabdo_ncap_2; 1.
SQ	SEQUENCE 391 AA; 42073 MW; 7F9F11640AA7AA6D CRC64;
Query Match	
Best Local Similarity 61.3%; Score 38; DB 12; Length 391;	
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	2 RPQGKLTk 9
Db	183 RPQGKLTk 190
RESULT 25	
ID	Q9QL89 PRELIMINARY; PRT; 392 AA.
AC	Q9QL89;
DT	01-MAY-2000 (TREMBlrel. 13, Created)
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE	Nucleocapsid protein.
OS	Hirame rhabdovirus.
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC	Rhabdoviridae; Novirhabdovirus.
NCBI_TaxID=38142;	
RN	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=CA 9703;
RC	Oh H.K., Choi T.J.;
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RA	EMBL; AF104985; AAF14116.1; -.
DR	GO; GO:0019013; C:Viral nucleocapsid; IEA.
DR	InterPro; IPR004902; Rhabdo_ncap_2.
DR	Pfam; PF03216; Rhabdo_ncap_2; 1.
SQ	SEQUENCE 392 AA; 42465 MW; C5A282238FC7A638 CRC64;
Query Match	
Best Local Similarity 61.3%; Score 38; DB 12; Length 392;	
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	2 RPQGKLTk 9
Db	182 RPQGKLTk 189
RESULT 26	
ID	Q9UFH0 PRELIMINARY; PRT; 417 AA.
AC	Q9UFH0;
DT	01-MAY-2000 (TREMBlrel. 13, Created)
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE	Hypothetical protein (fragment).
GN	DXFPZP434LI050.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;	
RN	[1]
RN	SEQUENCE FROM N.A.
RC	TISSUE=Testis;
RC	Tissuetestis;
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RA	PoustaKa A., Klein M., Mwes H.W., Gassenhuber J., Wiemann S.;

DR	EMBL; ALJ122079; CAB59254.1; -.
DR	NCBI_TaxID=11290;
RN	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=Round Butte 1;
RC	Emmenegger E.J., Kurath G.;
RL	Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RA	EMBL; U50402; AAA97895.1; -.
DR	GO; GO:0019013; C:Viral nucleocapsid; IEA.
DR	InterPro; IPR004902; Rhabdo_ncap_2.
DR	Pfam; PF03216; Rhabdo_ncap_2; 1.
SQ	SEQUENCE 391 AA; 42073 MW; 7F9F11640AA7AA6D CRC64;</

DR	EMBL; ALJ122079; CAB59254.1; -.
DR	NCBI_TaxID=11290;
RN	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=Round Butte 1;
RC	Emmenegger E.J., Kurath G.;
RL	Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RA	EMBL; U50402; AAA97895.1; -.
DR	GO; GO:0019013; C:Viral nucleocapsid; IEA.
DR	InterPro; IPR004902; Rhabdo_ncap_2.
DR	Pfam; PF03216; Rhabdo_ncap_2; 1.
SQ	SEQUENCE 391 AA; 42073 MW; 7F9F11640AA7AA6D CRC64;
Query Match	
Best Local Similarity 61.3%; Score 38; DB 12; Length 391;	
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	2 RPQGKLTG 9
Db	183 RPQGKLTG 190
RESULT 25	
ID	Q9QL89 PRELIMINARY; PRT; 392 AA.
AC	Q9QL89;
DT	01-MAY-2000 (TREMBlrel. 13, Created)
DT	01-JUN-2000 (TREMBlrel. 13, Last sequence update)
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE	Nucleocapsid protein.
OS	Hirame rhabdovirus.
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC	Rhabdoviridae; Novirhabdovirus.
NCBI_TaxID=38142;	
RN	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=CA 9703;
RC	Oh H.K., Choi T.J.;
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF104985; AAF14116.1; -.
DR	GO; GO:0019013; C:Viral nucleocapsid; IEA.
DR	InterPro; IPR004902; Rhabdo_ncap_2.
DR	Pfam; PF03216; Rhabdo_ncap_2; 1.
SQ	SEQUENCE 392 AA; 42465 MW; C5A282238FC7A638 CRC64;
Query Match	
Best Local Similarity 61.3%; Score 38; DB 12; Length 392;	
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	2 RPQGKLTG 9
Db	182 RPQGKLTG 189
RESULT 26	
ID	Q9UFH0 PRELIMINARY; PRT; 417 AA.
AC	Q9UFH0;
DT	01-MAY-2000 (TREMBlrel. 13, Created)
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE	Hypothetical protein (fragment).
GN	DXFPZP434LI050.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;	
RN	[1]
RN	SEQUENCE FROM N.A.
RC	TISSUES=Testis;
RC	Gloekner F.O., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.;
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

DR	EMBL; ALJ122079; CAB59254.1; -.
DR	NCBI_TaxID=11290;
RN	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=Round Butte 1;
RC	Emmenegger E.J., Kurath G.;
RL	Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RA	EMBL; U50402; AAA97895.1; -.
DR	GO; GO:0019013; C:Viral nucleocapsid; IEA.
DR	InterPro; IPR004902; Rhabdo_ncap_2.
DR	Pfam; PF03216; Rhabdo_ncap_2; 1.
SQ	SEQUENCE 391 AA; 42073 MW; 7F9F11640AA7AA6D CRC64;
Query Match	
Best Local Similarity 61.3%; Score 38; DB 12; Length 391;	
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	2 RPQGKLTG 9
Db	183 RPQGKLTG 190
RESULT 25	
ID	Q9QL89 PRELIMINARY; PRT; 392 AA.
AC	Q9QL89;
DT	01-MAY-2000 (TREMBlrel. 13, Created)
DT	01-JUN-2000 (TREMBlrel. 13, Last sequence update)
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE	Nucleocapsid protein.
OS	Hirame rhabdovirus.
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC	Rhabdoviridae; Novirhabdovirus.
NCBI_TaxID=38142;	
RN	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=CA 9703;
RC	Oh H.K., Choi T.J.;
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF104985; AAF14116.1; -.
DR	GO; GO:0019013; C:Viral nucleocapsid; IEA.
DR	InterPro; IPR004902; Rhabdo_ncap_2.
DR	Pfam; PF03216; Rhabdo_ncap_2; 1.
SQ	SEQUENCE 392 AA; 42465 MW; C5A282238FC7A638 CRC64;
Query Match	
Best Local Similarity 61.3%; Score 38; DB 12; Length 392;	
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	2 RPQGKLTG 9
Db	182 RPQGKLTG 189
RESULT 26	
ID	Q9UFH0 PRELIMINARY; PRT; 417 AA.
AC	Q9UFH0;
DT	01-MAY-2000 (TREMBlrel. 13, Created)
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE	Hypothetical protein (fragment).
GN	DXFPZP434LI050.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;	
RN	[1]
RN	SEQUENCE FROM N.A.
RC	TISSUES=Testis;
RC	Gloekner F.O., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.;
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

RT "Complete genome sequence of the marine planctomycete Pirellula sp.  
 RT strain 1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).  
 DR EMBL; BX294133; CAD71557.1; -;  
 KW Complete proteome.  
 SQ SEQUENCE 654 AA; 70834 MW; 2BC43E15FAD6AD87 CRC64;

Query Match 61.3%; Score 38; DB 16; Length 654;  
 Best Local Similarity 77.8%; Pred. No. 1.4e+02;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PQGQELTKQ 11  
 DB 446 PQGNLVKQ 454

RESULT 29

Q81WF8  
 ID Q81WF8 PRELIMINARY; PRT; 753 AA.  
 AC Q81WF8;  
 DT 01-WAR-2003 (TREMELrel. 23, Created)  
 DT 01-WAR-2003 (TREMELrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE Similar to hypothetical protein FLJ12892.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RA Strausberg R.;

RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC040285; AAH40285.1; -;  
 DR GO; GO:0005507; F:copper ion binding; IEA.  
 DR GO; GO:0005489; F:electron transporter activity; IEA.  
 DR GO; GO:0006118; F:electron transport; IEA.  
 DR InterPro; IPR000923; BlueCu 1.  
 DR PROSITE; PS00196; COPPER\_BLUE; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 753 AA; 83595 MW; 882A6B248030480C CRC64;

Query Match 61.3%; Score 38; DB 4; Length 753;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9  
 DB 461 CKPGNNLT 469

RESULT 30

Q94H84  
 ID Q94H84 PRELIMINARY; PRT; 780 AA.  
 AC Q94H84;  
 DT 01-DEC-2001 (TREMELrel. 19, Created)  
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Oryza sativa (Rice)  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Eriocaulaceae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Nipponbare;  
 RA Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,  
 RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,  
 RA Riggs F., Hsiao J., Ziemann V., Blunt S., Pai G., VanAken S.E.,  
 RA Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,  
 RA White O., Fraser C.M.;  
 RT "Oryza sativa chromosome 3 BAC OSJNBA0090P23 genomic sequence.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC084380; AAK52142.1; -;  
 DR Gramene; Q94H84; F:ATP binding; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000270; OPR\_PBI.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_Chk\_pkin\_AS.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00564; PBI; 1.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00666; PBI; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW Hypothetical protein; ATP-binding; Transferase.

SQ SEQUENCE 780 AA; 87258 MW; 6D4BB12E04F13F1E CRC64;

Query Match 61.3%; Score 38; DB 10; Length 780;  
 Best Local Similarity 77.8%; Pred. No. 1.7e+02;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RPQQELTKQ 10  
 DB 178 RPQELKQ 186

RESULT 31

Q723N3  
 ID Q723N3 PRELIMINARY; PRT; 793 AA.  
 AC Q723N3;  
 DT 01-OCT-2003 (TREMELrel. 25, Created)  
 DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE Hypothetical protein DKFZp686G1990.  
 GN DKFZP686G1990.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human retina;  
 RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,  
 RA Han M., Wiemann S.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX537652; CAD97804.1; -;  
 KW Hypothetical protein.

SQ SEQUENCE 793 AA; 88258 MW; AB0404EF5FAB5A39 CRC64;

Query Match 61.3%; Score 38; DB 4; Length 793;  
 Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9  
 DB 501 CKPGNNLT 509

RESULT 32

Q9U5P6  
 ID Q9U5P6 PRELIMINARY; PRT; 978 AA.  
 AC Q9U5P6;  
 DT 01-MAY-2000 (TREMELrel. 13, Created)  
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE Microsomal aminopeptidase.  
 GN H11-1.

```

OS Haemonchus contortus (Barber pole worm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
OX NCBI_TaxID=6289;
RN [1]
RP SEQUENCE FROM N.A.
RA Graham M., Smith T.S., Munn E.A., Coadwell W.J., Newton S.E.,
RA Barker P.J.;
RT "Cloning and sequencing of variants of H1L, the highly protective
RT membrane glycoprotein from Haemonchus contortus."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ249941; CAB57357.1; -.
DR MERO8; M01.015; -.
DR GO: GO:0004177; F:aminopeptidase activity; IEA.
DR GO: GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO: GO:0008237; F:metallopeptidase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001930; Peptidase M1.
DR InterPro: IPR006025; Pept M.Zn_BS.
DR Pfam: PF01433; Peptidase_M1; 1.
DR PRINTS; PR00756; ALADIPASE.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Aminopeptidase.
SQ SEQUENCE 978 AA; 112117 MW; D4615283D35AB8E7 CRC64;

Query Match 61.3%; Score 38; DB 5; Length 978;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELT 8
Db 788 CRPGQAT 795

RESULT 33
Q9JUS0 PRELIMINARY; PRT; 997 AA.
AC Q9JUS0;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Cegp1 protein.
GN CEGP1 OR CEGP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Bahr A., Hankeln T., Winterpacht A., Zabel B., Schmidt E.R.;
RT "Comparative sequencing of Human chromosome 11p15 and mouse chromosome
RT 7."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL: AJ400877; CAB92285.1; -.
DR HSP; P07204; IADX.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR InterPro: IPR000152; Asx_hydroxyl_S.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF_like.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00008; EGF; 7.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 6.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS01187; EGF_CA; 6.
KW EGF-like domain.
SQ SEQUENCE 997 AA; 109923 MW; B0261CD9C8F70701 CRC64;

Query Match 61.3%; Score 38; DB 5; Length 978;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELT 8
Db 788 CRPGQAT 795

RESULT 33
Q9JUS0 PRELIMINARY; PRT; 997 AA.
AC Q9JUS0;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Cegp1 protein.
GN CEGP1 OR CEGP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Bahr A., Hankeln T., Winterpacht A., Zabel B., Schmidt E.R.;
RT "Comparative sequencing of Human chromosome 11p15 and mouse chromosome
RT 7."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL: AJ400877; CAB92285.1; -.
DR HSP; P07204; IADX.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR InterPro: IPR000152; Asx_hydroxyl_S.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF_like.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00008; EGF; 9.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 6.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS01187; EGF_CA; 6.
KW EGF-like domain.
SQ SEQUENCE 997 AA; 109923 MW; B0261CD9C8F70701 CRC64;

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Query Match 61.3%; Score 38; DB 11; Length 997;
Best Local Similarity 77.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
Db 198 CRPGFELAK 206

RESULT 34
Q9NQ36 PRELIMINARY; PRT; 999 AA.
ID Q9NQ36
AC Q9NQ36;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE CEGP1 protein.
GN CEGP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bahr A., Hankeln T., Winterpacht A., Zabel B., Schmidt E.R.;
RT "Comparative sequencing of Human chromosome 11p15 and mouse chromosome
RT 7."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL: AJ400877; CAB92285.1; -.
DR HSP; P07204; IADX.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR InterPro: IPR000152; Asx_hydroxyl_S.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF_like.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00008; EGF; 7.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 6.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS01187; EGF_CA; 6.
KW EGF-like domain.
SQ SEQUENCE 999 AA; 109956 MW; 61334844A0053095 CRC64;

Query Match 61.3%; Score 38; DB 4; Length 999;
Best Local Similarity 77.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9
Db 200 CRPGFELAK 208

RESULT 35
Q9LPK1 PRELIMINARY; PRT; 1207 AA.
ID Q9LPK1
AC Q9LPK1;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE FeN18.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,

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RA Shinn P., Altrafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,  
 RA Conway A., Gonzales A., Hansen N., Hong B., Koo T., Lam B., Lee J.,  
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharisky N., Nguyen M.,  
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,  
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,  
 RA Ecker J.R.;  
 RT "Genomic sequence for Arabidopsis thaliana BAC F6N18 from chromosome  
 I";  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC017118; AAF2964.2; -;  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0004289; F:subtilase activity; IEA.  
 DR GO; GO:0006310; P:DNA recombination; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000209; Peptidase\_S8.  
 DR InterPro; IPR001584; Rve.  
 DR InterPro; IPR001878; Znf\_CCHC.  
 DR Pfam; PF00665; rve; 1.  
 DR Pfam; PF00098; zf-CCHC; 1.  
 DR PRINTS; PR00939; C2HCZNFINGER.  
 DR SMART; SM00343; Znf\_C2HC; 1.  
 DR SMART; SM00343; Znf\_C2HC; 1.  
 DR PROSITE; PS00136; SUBTILASE\_ASP; 1.  
 DR PROSITE; PS0158; ZF\_CCHC; 1.  
 DR PROSITE; PS0158; ZF\_CCHC; 1.  
 SQ SEQUENCE 1207 AA; 138738 MW; 60328FAE6B25A150 CRC64;

Query Match 61.3%; Score 38; DB 10; Length 1207;  
 Best Local Similarity 77.8%; Pred. No. 2.6e+02;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PGQELTKQG 11  
 Db 1001 PGQKUTKAG 1009

RESULT 36  
 Q9C7Y1 PRELIMINARY; PRT; 1334 AA.  
 AC Q9C7Y1; 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Copia-type polypeptide, putative.  
 GN T9G5.7  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016719; PubMed=11130712;  
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
 RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,  
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
 RA Chung M.K., Conn A., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
 RA Dunn P., Egtu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,  
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
 RA Kim C.J., Koo H.B., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,  
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani A.,  
 RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
 RA Uteback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,  
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
 thaliana";  
 RL Nature 408:816-820(2000).  
 DR EMBL; AC055769; AAG51247.1; -;  
 DR PIR; E86451; E86451.

DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0004289; F:subtilase activity; IEA.  
 DR GO; GO:0006310; P:DNA recombination; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000209; Peptidase\_S8.  
 DR InterPro; IPR001584; Rve.  
 DR InterPro; IPR001878; Znf\_CCHC.  
 DR Pfam; PF00665; rve; 1.  
 DR Pfam; PF00098; zf-CCHC; 1.  
 DR PRINTS; PR00939; C2HCZNFINGER.  
 DR SMART; SM00343; Znf\_C2HC; 1.  
 DR PROSITE; PS00136; SUBTILASE\_ASP; 1.  
 DR PROSITE; PS0158; ZF\_CCHC; 1.  
 DR PROSITE; PS0158; ZF\_CCHC; 1.  
 SQ SEQUENCE 1334 AA; 153488 MW; A5718931BC7BD021 CRC64;  
 Query Match 61.3%; Score 38; DB 10; Length 1334;  
 Best Local Similarity 77.8%; Pred. No. 2.9e+02;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 PGQELTKQG 11  
 Db 1096 PGQKUTKAG 1104

RESULT 37  
 Q9FH39 PRELIMINARY; PRT; 1334 AA.  
 AC Q9FH39; 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Copia-type polypeptide.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Columbia;  
 RX MEDLINE=20181125; PubMed=10718197;  
 RA Sato S., Nakamura Y., Kaneko T., Katch T., Asamizu E., Kotani H.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence  
 RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC  
 RT clones";  
 RN DNA Res. 7:31-63(2000).  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Columbia;  
 RX MEDLINE=21219200; PubMed=11319272;  
 RA Terol J., Castillo M.C., Bagues M., Perez-Alonso M., de Frutos R.;  
 RT "Structural and evolutionary analysis of the copia-like elements in  
 RT the Arabidopsis thaliana genome";  
 RL Mol. Biol. Evol. 18:882-892(2001).  
 DR EMBL; AB022213; BAB1200.1; -;  
 DR EMBL; AJ292423; CAC37622.1; -;  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0004289; F:subtilase activity; IEA.  
 DR GO; GO:0006310; P:DNA recombination; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000209; Peptidase\_S8.  
 DR InterPro; IPR001584; Rve.  
 DR InterPro; IPR001878; Znf\_CCHC.  
 DR Pfam; PF00665; rve; 1.  
 DR Pfam; PF00098; zf-CCHC; 1.  
 DR PRINTS; PR00939; C2HCZNFINGER.  
 DR SMART; SM00343; Znf\_C2HC; 1.  
 DR PROSITE; PS00136; SUBTILASE\_ASP; 1.  
 DR PROSITE; PS0158; ZF\_CCHC; 1.  
 DR PROSITE; PS0158; ZF\_CCHC; 1.  
 SQ SEQUENCE 1334 AA; 153430 MW; 49A18931BC7BD0AC CRC64;

Query Match 61.3%; Score 38; DB 10; Length 1334;  
Best Local Similarity 77.8%; Pred. No. 2.9e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PQQLTKQG 11  
Db 1096 PQQLTKAG 1104

RESULT 38  
Q8H326 PRELIMINARY; PRT; 1335 AA.  
ID Q8H326  
AC Q8H326  
DT 01-MAR-2003 (T-EMBLrel. 23, Created)  
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
DE P059G07.2 protein.  
GN P059G07.2.  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoidae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Nipponbare;  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC  
clone:P0597G07";  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP004316; BAC16036.1; -.  
DR GO; GO:0005622; C:intracellular; IEA.  
DR InterPro; IPR001357; BRCT.  
DR Pfam; PF00533; BRCT; 3.  
DR SMART; SM00292; BRCT; 4.  
DR PROSITE; PS50172; BRCT; 3.  
SQ SEQUENCE 1335 AA; 145373 MW; 2656CEB046F34B0D CRC64;

Query Match 61.3%; Score 38; DB 10; Length 1335;  
Best Local Similarity 66.7%; Pred. No. 2.9e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPQELTK 9  
Db 1277 CKPQSLNK 1285

RESULT 39  
Q24406 PRELIMINARY; PRT; 110 AA.  
ID Q24406  
AC Q24406  
DT 01-NOV-1996 (T-EMBLrel. 01, Created)  
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
DE Protamine.  
GN MST35BB OR CG4478.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=OREGON R;  
RA Russell S.R.;  
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z46785; CAA86737.1; -.  
DR PIR; S52158; S52158.  
DR FlyBase; FBgn0013301; Mst35Bb.  
SQ SEQUENCE 110 AA; 12329 MW; F77095E39F543B20 CRC64;

Query Match 59.7%; Score 37; DB 5; Length 110;  
Best Local Similarity 54.5%; Pred. No. 32;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Best Local Similarity 54.5%; Pred. No. 32;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPQELTKQG 11  
Db 69 CAPSQKCSKQG 79

RESULT 40  
Q24402 PRELIMINARY; PRT; 110 AA.  
ID Q24402  
AC Q24402  
DT 01-NOV-1996 (T-EMBLrel. 01, Created)  
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
DE Protamine.  
GN MST35BB OR CG4478.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=OREGON R;  
RA Russell S.R.;  
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z46784; CAA86736.1; -.  
DR PIR; S52156; S52156.  
DR FlyBase; FBgn0013301; Mst35Bb.  
SQ SEQUENCE 110 AA; 12415 MW; B46395E39F4A1DFB CRC64;

Query Match 59.7%; Score 37; DB 5; Length 110;  
Best Local Similarity 54.5%; Pred. No. 32;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPQELTKQG 11  
Db 69 CAPSQKCSKQG 79

Search completed: May 5, 2004, 14:40:34  
Job time : 4.76712 secs



OM protein - protein search, using sw model

Run on: May 5, 2004, 14:30:20 ; Search time 12.4144 Seconds  
(without alignments)  
568,992 Million cell updates/sec

Title: US-10-067-122B-2\_COPY\_133\_157

Perfect score: 139  
Sequence: 1 CRPWTNCSLDGRSVLKGTGTEDV 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 292547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	139	100.0	191	4 AAB66986	Aab66986 41bb prot
2	139	100.0	256	2 AAR64199	Aar64199 Murine 4-
3	139	100.0	256	2 AAR70978	Aar70978 4-1BB rec
4	139	100.0	256	2 AAW04173	Aaw04173 Mouse rec
5	139	100.0	256	2 AAW26659	Aaw26659 Mouse 4-1
6	139	100.0	256	2 AAY28687	Aay28687 Mouse Rec
7	139	100.0	256	2 AAY33215	Aay33215 Murine CD
8	139	100.0	256	5 AAE22581	Aae22581 Mouse rec
9	139	100.0	256	5 ABB75954	Abb75954 Murine cy
10	139	100.0	256	7 ADC25939	Adc25939 Murine re
11	139	100.0	256	7 ADE87549	Ade87549 Mouse rec
12	115	82.7	132	3 AAY94714	Aay94714 Tumour ne
13	115	82.7	219	2 AAW31759	Aaw31759 A novel h
14	115	82.7	219	2 AAW92523	Aaw92523 Human h4-
15	115	82.7	219	2 AAW92524	Aaw92524 Human h4-
16	115	82.7	219	4 AAE08545	Aae08545 Human h4-
17	115	82.7	219	6 ABB84639	Abb84639 Human h4-
18	115	82.7	255	2 AAR74087	Aar74087 Human rec
19	115	82.7	255	2 AAR64197	Aar64197 Human 4-1
20	115	82.7	255	2 AAR70977	Aar70977 H4-1BB re
21	115	82.7	255	2 AAW26658	Aaw26658 Human 4-1
22	115	82.7	255	2 AAY28688	Aay28688 Human rec
23	115	82.7	255	2 AAY33214	Aay33214 Human CD1
24	115	82.7	255	4 AAE08546	Aae08546 Human h4-
25	115	82.7	255	4 AAB50521	Aab50521 Human tum

26	115	82.7	255	5 ABB75955	Abb75955 Human cyt
27	115	82.7	255	6 ABR39863	Abbr39863 Human MOC
28	115	82.7	255	6 ABB84640	Abb84640 Human h4-
29	115	82.7	255	7 AAE39531	Aae39531 Human pro
30	115	82.7	255	7 ADC78803	Adc78803 Human PRO
31	115	82.7	255	7 ADD25599	Add25599 Binding d
32	115	82.7	255	7 ADE87541	Ade87541 Unknown h
33	102	73.4	255	2 AAW04174	Aaw04174 Human rec
34	86	61.9	201	3 AAY59508	Aay59508 OBM bindi
35	86	61.9	443	7 ADB17000	Adb17000 Murine RA
36	86	61.9	625	2 AAW83200	Aaw83200 Murine os
37	86	61.9	625	2 AAW69958	Aaw69958 Murine NF
38	86	61.9	625	2 AAW68294	Aaw68294 Murine NF
39	86	61.9	625	2 AAE08739	Aae08739 Murine re
40	86	61.9	625	3 AAY53649	Aay53649 A mouse r
41	86	61.9	625	3 AAY59509	Aay59509 OBM bindi
42	86	61.9	625	4 AAE04427	Aae04427 Murine re
43	86	61.9	625	4 AAE01994	Aae01994 Murine RA
44	86	61.9	625	5 AAE26104	Aae26104 Mouse RAN
45	86	61.9	625	6 ABP58179	Abp58179 Murine RA

ALIGNMENTS

RESULT 1  
AAB66986  
ID AAB66986 standard; protein; 191 AA.

XX AAB66986;  
AC  
DT 19-APR-2001 (first entry)  
XX  
DE 41bb protein.  
XX  
KW Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;  
KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;  
KW systemic lupus erythematosus; graft-versus-host disease; septic shock;  
KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;  
KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;  
KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;  
KW ischaemia; Parkinson's disease.  
XX  
OS Unidentified.  
XX  
PN WO200103719-A2.  
XX  
PD 18-JAN-2001.  
XX  
XX 07-JUL-2000; 2000WO-US018667.  
XX  
XX 09-JUL-1999; 99US-00350670.  
XX  
XX 09-DEC-1999; 99US-00457647.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Boyle WT, Lacey DL, Calzone FJ, Chang M, Senaldi G;  
XX  
XX WPI; 2001-103031/11.  
XX  
XX Treating conditions leading to bone loss such as rheumatoid arthritis,  
XX multiple sclerosis and asthma, comprises administering an osteoprotegerin  
XX protein in conjunction with e.g. inhibitors of interleukin and tumor  
XX necrosis factor alpha.  
XX  
XX Disclosure; Fig 2; 316pp; English.  
XX  
XX The present invention relates to a method for treating conditions leading  
XX to bone loss. The method comprises administering a purified and isolated  
XX osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)  
XX in conjunction with other substances such as tumour necrosis factor-alpha  
XX (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE  
XX modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet

CC activating factor (PAF) antagonists. The method is useful for treating  
 CC conditions leading to bone loss such as rheumatoid arthritis, multiple  
 CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also  
 CC useful for treating inflammation, systemic lupus erythematosus (SLE) and  
 CC graft-versus-host disease (GVHD). Other diseases that can be treated  
 CC include acute pancreatitis, Alzheimer's disease, anorexia,  
 CC atherosclerosis, coronary conditions (e.g. myocardial infarction),  
 CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,  
 CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,  
 CC psoriasis and septic shock. The present sequence was used in a sequence  
 CC homology comparison  
 XX  
 XX Sequence 191 AA;

SQ

Query Match 100.0%; Score 139; DB 4; Length 191;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-13;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
 Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 2

AAAR64199  
 ID AAR64199 standard; protein; 256 AA.

XX AC AAR64199;

XX XX 25-MAR-2003 (revised)

DT 08-AUG-1995 (first entry)

XX DE Murine 4-1BB polypeptide.

XX T-cell; lymphocyte; activation; tissue culture; clone; cell lines;  
 KW proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine.  
 XX  
 XX Mus musculus.

XX PN WO9426290-A1.

XX PD 24-NOV-1994.

XX PF 06-MAY-1994; 94WO-US005036.

XX PR 07-MAY-1993; 93US-00060843.

XX PA (IMV ) IMMUNEX CORP.

XX PI Goodwin RG, Smith CA, Alderson MR;

XX DR WPI; 1995-022265/03.

XX DR N-PSDB; AAQ75428.

XX Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor 4-1BB  
 PT to transduce signal.  
 XX

PS Example 1; Page 44-45; 65pp; English.

XX The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see AAQ75422)  
 CC are useful in a pharmaceutical composition for stimulating the immune  
 CC system. The 4-1BB and 4-1BB-L polypeptides are also useful for exploring  
 CC mechanisms of T-cell activation, as they are expressed on T lymphocytes.  
 CC 4-1BB-L can be used as a tissue culture reagent for in vitro cultivation  
 CC of primary T-cells during the derivation of clonal T-cell lines. It may  
 CC also be used to stimulate proliferation of activated T-cells, used in  
 CC therapeutic procedures. (Updated on 25-MAR-2003 to correct PN field.)  
 XX

SQ Sequence 256 AA;

Query Match 100.0%; Score 139; DB 2; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-12;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
 Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 3

AAAR70978  
 ID AAR70978 standard; protein; 256 AA.

XX AC AAR70978;

XX XX 25-MAR-2003 (revised)

DT 16-OCT-1995 (first entry)

XX DE 4-1BB receptor protein.

XX 4-1BB; receptor protein; immunosuppressive; autoimmune disease;  
 KW organ transplantation; cell membrane ligand.  
 XX  
 XX Mus sp.

XX PH Key

FT Peptide

XX Location/Qualifiers

XX 1..23

XX /label= Sig\_peptide

XX PN WO9507984-A1.

XX PD 23-MAR-1995.

XX PF 15-SEP-1994; 94WO-US010457.

XX PR 16-SEP-1993; 93US-00122796.

XX PA (INDV ) UNIV INDIANA FOUND.

XX PI Kwon BS;

XX DR WPI; 1995-131352/17.

XX DR N-PSDB; AAQ86127.

XX Novel cDNA encoding human receptor protein H4-1BB - useful to produce the  
 PT protein which is used to treat autoimmune disease and facilitate organ  
 PT transplantation.

XX PS Disclosure; Fig 1; 36pp; English.

XX CC cDNA encoding the human receptor protein H4-1BB (given in AAQ86126) was  
 CC isolated using PCR primers based on the homologous mouse 4-1BB gene  
 CC (AAQ86127) encoding mouse receptor protein (AAR70978). (Updated on 25-MAR  
 CC -2003 to correct PN field.)  
 XX

SQ Sequence 256 AA;

Query Match 100.0%; Score 139; DB 2; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-12;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
 Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 4

AAW04173  
 ID AAW04173 standard; protein; 256 AA.

XX AC AAW04173;

XX DT 12-DEC-1996 (first entry)

XX XX Mouse receptor 4-1BB.

XX



KW Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;  
KW immunostimulant; cancer; autoimmune disease; graft rejection; therapy.  
XX Mus sp.  
XX WO9629348-A1.  
XX PD 26-SEP-1996.  
XX 22-MAR-1996; 96WO-US003965.  
XX 23-MAR-1995; 95US-00409851.  
XX (INDV ) UNIV INDIANA FOUND.  
XX Kwon BS, Kang C;  
XX WPI; 1996-443138/44.  
XX N-PSDB; AAT39541.  
XX Monoclonal antibody specific for human receptor protein 4-1BB - used to  
PT enhance proliferation and activation of T-cells for treatment of cancer  
PT and to inhibit specific ligand binding for treating auto-immune diseases.  
XX Disclosure; Page 32-34; 48pp; English.  
XX Novel murine receptor protein 4-1BB (AAW04173) has the potential to  
CC function as an accessory signaling molecule during T-cell activation and  
CC proliferation. It may represent a cell surface molecule involved in T-  
CC cell-APC interactions and may also act as a B-cell costimulator. It is  
CC structurally related to members of the nerve growth factor receptor  
CC superfamily. Its amino acid sequence was deduced from an isolated cDNA  
CC clone (see also AAT39541). A human homologue, H4-1BB (AAW04174), was  
CC identified and used to raise a monoclonal antibody useful in cancer and  
CC autoimmune disease therapy  
XX Sequence 256 AA;  
SQ

Query Match 100.0%; Score 139; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. NO. 1.4e-12;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 5  
AAW26659  
ID AAW26659 standard; protein; 256 AA.  
XX AAW26659;  
XX 25-MAR-2003 (revised)  
DT 25-FEB-1998 (first entry)  
XX Mouse 4-1BB receptor.  
DE  
XX 4-1BB ligand; 4-1BB-L; receptor; mouse; cytokine; T lymphocyte; T cell;  
KW proliferation; immunostimulant.  
XX Mus musculus.  
XX  
XX Key Location/Qualifiers  
FT Peptide 1..23  
FT /label= Sig\_peptide  
XX US5674704-A.  
XX 07-OCT-1997.  
XX 06-MAY-1994; 94US-00236918.  
XX

PR 07-MAY-1993; 93US-00060843.  
XX (IMMV ) IMMUNEX CORP.  
XX Alderson MR, Goodwin RG, Smith CA;  
XX WPI; 1997-502333/46.  
XX N-PSDB; AAT91027.  
XX DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating T-cell  
PT proliferation in vitro, and as research tools.  
XX Disclosure; Col 39-40; 32pp; English.  
XX This protein comprises mouse 4-1BB, a member of the tumour necrosis  
CC factor receptor superfamily that is expressed on helper, suppressor and  
CC cytolytic T cells, as well as on mouse brain tissue. A novel claimed  
CC cytokine, designated 4-1BB ligand (4-1BB-L) has been identified, cloned  
CC and sequenced (see AAW26656) that binds to murine 4-1BB, 4-1BB-L, late T-  
CC especially its soluble extracellular domain, can be used to stimulate T-  
CC cell proliferation in vitro, as a research tool and as an affinity ligand  
CC for purifying 4-1BB. (Updated on 25-MAR-2003 to correct PF field.)  
XX Sequence 256 AA;  
SQ

Query Match 100.0%; Score 139; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. NO. 1.4e-12;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 6  
AAW28687  
ID AAW28687 standard; protein; 256 AA.  
XX AAW28687;  
XX 13-OCT-1999 (first entry)  
XX Mouse Receptor 4-1BB protein.  
DE  
XX Mouse Receptor 4-1BB cDNA; Mouse Receptor 4-1BB protein; H4-1BB protein;  
KW human 4-1BB protein; T cell activation; proliferation; immune response;  
KW receptor protein; autoimmune disease; organ transplantation;  
KW cancerous tumour; nerve growth factor receptor.  
XX Mus musculus.  
XX WO9936093-A1.  
XX 22-JUL-1999.  
XX 14-JAN-1999; 99WO-US000823.  
XX 14-JAN-1998; 98US-00007097.  
XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.  
XX (KWON/) KWON B S.  
XX Kwon BS;  
XX WPI; 1999-444325/37.  
XX N-PSDB; AAX90763.  
XX Using human receptor protein 4-1BB ligands to, e.g. treat Diabetes  
PT Mellitus, Rheumatoid Arthritis and Systemic Lupus Erythematosus.  
XX Disclosure; Page 75; 86pp; English.  
XX The present sequence is mouse 4-1BB receptor protein. This protein has  
CC

CC 65% homology with human receptor protein 4-1BB. The protein has a  
 CC putative leader sequence, a potential membrane anchor segment and other  
 CC features of known receptor proteins. 4-1BB is structurally related to  
 CC members of the nerve growth factor receptor. Probes derived from mouse 4-  
 CC 1BB cDNA are used to isolate cDNA of H4-1BB. The H4-1BB protein, its  
 CC ligands, and various monoclonal antibodies have therapeutic uses. They  
 CC may be used to enhance or suppress T cell activation and proliferation;  
 CC for activation or inhibition of immune response; to block H4-1BB ligand  
 CC binding; treating cancerous tumours and autoimmune diseases; and during  
 CC organ transplantation  
 XX  
 XX Sequence 256 AA;

Query Match 100.0%; Score 139; DB 2; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-12;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
 |||||  
 Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 7  
 AAY33215  
 ID AAY33215 standard; protein; 256 AA.  
 AC AAY33215;  
 XX  
 XX 18-NOV-1999 (first entry)  
 DE Murine CD137 protein.  
 DE  
 DE CD137; monocyte growth factor; proliferation; peripheral monocyte;  
 KW treatment; disease; antitumor; antibacterial; antiviral; antifungal;  
 KW immunostimulatory; non-specific immune response; phagocytosis;  
 KW intracellular destruction; microorganism; immune complex; antibody;  
 KW cytotoxicity; tumor cell; macrophage; hematopoietic system; leucopenia;  
 KW chemotherapy; radiation; therapy; wound healing disorder; tumor; fungal;  
 KW bacterial; viral infection; immunosuppressant; gene therapy; murine.

OS Mus sp.  
 XX WO9944629-A2.  
 PN 10-SEP-1999.  
 XX  
 XX 05-MAR-1999; 99WO-EP001440.  
 PF  
 XX 05-MAR-1998; 98EP-00103859.  
 PR  
 XX (MERC ) MERCKLE GMBH.  
 PA  
 PI Schwarz H, Langstein J;  
 XX  
 XX WPI; 1999-550983/46.  
 DR  
 XX Use of monocyte growth factor CD137 for stimulating proliferation of  
 PT peripheral monocytes, particularly for treating immune deficiency, e.g.  
 PT following cancer therapy.  
 XX  
 XX Disclosure; Fig 1B; 57pp; German.

CC This invention describes a novel use of the human monocyte growth factor  
 CC CD137, or its functional analogs, for (i) stimulating proliferation of  
 CC peripheral monocytes; and (ii) treating diseases that are associated with  
 CC disorders of a cellular system that includes monocytes (and/or their  
 CC derived cells, precursor or progenitors) or where the origin and/or  
 CC progression is treatable by stimulating proliferation of such cells. The  
 CC products of the invention have antitumor, antibacterial, antiviral,  
 CC antifungal and immunostimulatory activity. Stimulating proliferation of  
 CC monocytes promotes the non-specific immune response, i.e. it increases  
 CC phagocytosis and intracellular destruction of microorganisms, immune  
 CC complexes and damaged cells, and improves antibody (in)dependent

CC cytotoxicity to tumor cells. CD137 is used, in vivo or ex vivo, to treat  
 CC diseases associated with a defective immune response where caused by  
 CC inadequate numbers of active monocytes/macrophages, especially damage to  
 CC the hematopoietic system (leucopenia) caused by chemotherapy or radiation  
 CC therapy; disorders of wound healing (e.g. in dialysis or diabetic  
 CC patients, or those with chronic venous insufficiency); tumors; bacterial,  
 CC fungal or viral infections; (non-)congenital or (non-)inherited diseases  
 CC or injury to the immune system; injury induced by treatment with  
 CC immunosuppressants (e.g. patients with chronic arthritis or autoimmune  
 CC disease, or transplant patients). Nucleic acid encoding (i) can be used  
 CC similarly, in gene therapy procedures. Proliferation of peripheral  
 CC monocytes is achieved independently of hematopoietic stem cells. This  
 CC sequence represents the murine CD137 protein described in the method of  
 CC the invention  
 XX  
 XX Sequence 256 AA;

Query Match 100.0%; Score 139; DB 2; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-12;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
 |||||  
 Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 8  
 AAE22581  
 ID AAE22581 standard; protein; 256 AA.  
 AC AAE22581;  
 XX  
 XX 26-JUL-2002 (first entry)  
 DE Mouse receptore 4-1BB protein.  
 DE  
 DE Mouse; lymphokine; L2G25B; macrophage inflammatory protein 1 alpha;  
 KW MIP-1alpha; immune disease; myeloid progenitor cell differentiation;  
 KW 4-1BB; receptor.  
 XX

OS Mus sp.  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1..22  
 FT /label= Signal\_peptide  
 FT Protein 23..256  
 FT /note= "Mature receptor 4-1BB protein"  
 FT Modified-site 128..130  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 138..140  
 FT /note= "Asn is N-glycosylated"

PN US6355476-B1.  
 XX  
 XX 12-MAR-2002.  
 PD  
 XX 30-JUL-1992; 92US-00922996.  
 PF  
 XX 07-NOV-1988; 88US-00267577.  
 PR  
 XX (ADRE-) ADVANCED RES & TECHNOLOGY INC.

XX Kwon BS, Broxmeyer HE;  
 PI WPI; 2002-370577/40.  
 DR N-PSDB; AAD35694.  
 DR  
 XX New isolated and purified cDNA designated L25G25B encoding the mouse  
 PT lymphokine macrophage inflammatory protein 1 alpha which can be used for  
 PT modulating early myeloid progenitor cell differentiation.  
 XX  
 XX Disclosure; Fig 3; 81pp; English.

CC The invention relates to an isolated and purified cDNA containing mouse  
CC lymphokine designated L2G25B. L2G25B cDNA encodes lymphokine macrophage  
CC inflammatory protein 1 alpha (MIP-1alpha). Lymphokines are proteins by  
CC which the immune cells communicate with each other. Lymphokines are used  
CC therapeutically against immunologic diseases. Mouse lymphokines MIP-alpha  
CC can be used to modulate early myeloid progenitor cell differentiation.  
CC The present sequence is mouse lymphokine receptor 4-1BB protein  
XX  
SQ Sequence 256 AA;  
Query Match 100.0%; Score 139; DB 5; Length 256;  
Best Local Similarity 100.0%; Pred. No. 1.4e-12; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0;  
Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157  
RESULT 9  
ABB75954  
ID ABB75954 standard; protein; 256 AA.  
AC ABB75954;  
XX  
XX 12-JUL-2002 (first entry)  
XX Murine cytokine receptor 4-1BB.  
DE  
XX Cytokine; receptor; 4-1BB; mouse.  
XX  
XX Mus sp.  
XX  
XX Key Location/Qualifiers  
XX Peptide 1..23  
XX Protein /label= Signal\_peptide  
XX 24..256  
XX /label= Mature\_protein  
XX  
XX US6355779-B1.  
XX  
XX 12-MAR-2002.  
XX  
XX 10-SEP-1998; 98US-00150864.  
XX  
XX 07-MAY-1993; 93US-00060843.  
XX  
XX 06-MAY-1994; 94US-00236918.  
XX  
XX 05-AUG-1997; 97US-00910449.  
XX  
XX (IMV ) IMMUNEX CORP.  
XX  
XX Goodwin RG, Smith CA, Alderson MR;  
XX  
XX WPI; 2002-380940/41.  
XX N-PSDB; ABL54047.  
XX  
XX New antibody specific for the cytokine 4-1BB-ligand, useful for  
XX immunocaffinity purification of the ligand.  
XX  
XX Example 1; Col 39-40; 31pp; English.  
XX  
XX The present sequence is the protein sequence of the murine cytokine  
XX receptor, 4-1BB. A portion of the extracellular (ligand binding) domain  
XX of the receptor was utilised in a murine 4-1BB/human IgG1 Fc fusion  
XX protein, which was used to identify the murine 4-1BB ligand (4-1BB-L, see  
XX ABB75952). The invention provides novel murine and human 4-1BB-L  
XX polypeptides and human 4-1BB polypeptides, as well as DNA sequences  
XX encoding them, recombinant expression vectors and host cells, and methods  
XX for producing the novel polypeptides by cultivating the transformed host  
XX cells. Soluble forms of the 4-1BB-L and 4-1BB polypeptides, derived from  
XX their extracellular domains, have therapeutic value. Antibodies that are  
XX immunoreactive with 4-1BB-L or human 4-1BB are claimed

SQ Sequence 256 AA;  
Query Match 100.0%; Score 139; DB 5; Length 256;  
Best Local Similarity 100.0%; Pred. No. 1.4e-12;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157  
RESULT 10  
ADC25939  
ID ADC25939 standard; protein; 256 AA.  
XX  
XX AC ADC25939;  
XX  
XX DT 18-DEC-2003 (first entry)  
XX  
XX Murine receptor 4-1BB protein.  
DE  
XX receptor 4-1BB; immunostimulant; B-cell activation; T-cell proliferation;  
XX cancer; murine; mouse.  
XX  
XX Mus musculus.  
XX  
XX US2003100745-A1.  
XX  
XX PD 29-MAY-2003.  
XX  
XX PF 04-FEB-2002; 2002US-00067122.  
XX  
XX PR 07-NOV-1988; 88US-00267577.  
XX  
XX PR 30-JUL-1992; 92US-00922996.  
XX  
XX PR 01-FEB-1993; 93US-00012269.  
XX  
XX PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.  
XX  
XX PI Kwon BS;  
XX  
XX WPI; 2003-678138/64.  
XX N-PSDB; ADC25938.  
XX  
XX New cDNA gene encoding receptor protein 4-1BB, useful for isolating  
XX similar DNA sequences, and the encoded polypeptide and an antibody to it,  
XX useful for identifying ligands, and for modulating immune cell activity.  
XX  
XX Claim 7; Fig 2; 77pp; English.  
XX  
XX The invention relates to a novel cDNA gene encoding receptor protein 4-  
XX 1BB. The cDNA gene of the invention demonstrates immunostimulant  
XX activities and may be useful as a probe to isolate DNA sequences encoding  
XX for proteins similar to the receptor protein encoded by the DNA. The  
XX protein, its fragments and derivatives may be useful as a probe to  
XX isolate ligands to receptor protein 4-1BB, for stimulating proliferation  
XX of B cells expressing 4-1BB ligands and for blocking 4-1BB ligand  
XX binding. The antibody may be useful for enhancing T-cell proliferation or  
XX activation. Finally, the invention may be useful with respect to cancer  
XX research. The current sequence is that of the murine receptor 4-1BB  
XX protein of the invention.  
XX  
SQ Sequence 256 AA;  
Query Match 100.0%; Score 139; DB 7; Length 256;  
Best Local Similarity 100.0%; Pred. No. 1.4e-12;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157  
RESULT 11

AD87549  
 ID ADE87549 standard; protein; 256 AA.  
 XX  
 AC ADE87549;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Mouse receptor H4-1BB.  
 XX  
 XX immunosuppressive; H4-1BB ligand binding blocker; mouse;  
 XX receptor protein; H4-1BB; B-cell proliferation stimulator;  
 KW T-cell proliferation enhancer; immune system suppressor; transplantation;  
 KW autoimmune disease.  
 XX  
 OS Mus sp.  
 XX  
 XX US2003082157-A1.  
 XX  
 XX 01-MAY-2003.  
 XX  
 XX 12-JUN-2002; 2002US-00170997.  
 XX  
 XX 07-NOV-1988; 89US-00267577.  
 PR 30-JUL-1992; 92US-00922996.  
 PR 01-FEB-1993; 93US-00012269.  
 PR 05-JUN-1995; 95US-00460976.  
 PR 22-OCT-1997; 97US-00955573.  
 XX  
 PA (KWON/) KWON B S.  
 XX  
 XX Kwon BS;  
 XX  
 XX WPI; 2003-576599/54.  
 DR N-PSDB; ADE87548.  
 XX  
 XX New cDNA, or its encoded receptor protein H4-1BB, useful as probes to  
 PT isolate DNAs or ligands to the receptor protein H4-1BB, or for blocking  
 PT H4-1BB ligand binding to facilitate organ transplantation or treat  
 PT autoimmune diseases.  
 XX  
 XX Disclosure; Fig 1; 19pp; English.  
 XX  
 XX The invention describes a cDNA, which encodes for human receptor protein  
 CC H4-1BB. The cDNA, or its fragments or derivatives, are useful as a probe  
 CC to isolate DNA sequences encoding for proteins similar to the receptor  
 CC protein H4-1BB. The receptor protein H4-1BB, or its fragments or  
 CC derivatives, is useful as a probe for identifying ligands to the receptor  
 CC protein H4-1BB, or for stimulating the proliferation of B-cells  
 CC expressing H4-1BB ligands. The monoclonal antibodies against H4-1BB are  
 CC useful for enhancing T-cell proliferation of activation. The cDNA or  
 CC receptor protein H4-1BB is also useful for blocking H4-1BB ligand  
 CC binding, which is particularly useful for suppressing the immune system  
 CC during transplantation, or for treating autoimmune diseases. This is the  
 CC amino acid sequence of mouse receptor H4-1BB.  
 XX  
 SQ Sequence 256 AA;  
 Query Match 100.0%; Score 139; DB 7; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-12;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
 DB 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157  
 RESULT 12  
 ID AAY94714  
 XX AAY94714 standard; protein; 132 AA.  
 AC AAY94714;  
 XX  
 XX 29-JAN-2001 (first entry)  
 DT

XX Tumour necrosis factor receptor (TNFR) domain of 4-1BB protein.  
 DE  
 XX  
 KW Tumour necrosis factor-receptor related protein; TR2; human; cancer;  
 KW chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease;  
 KW immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID;  
 KW severely combined immunodeficiency; apoptosis inhibition;  
 KW Alzheimer's disease; Parkinson's disease; Crohn's disease.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO2000056405-A2.  
 PN  
 XX 28-SEP-2000.  
 PD  
 XX  
 XX 22-MAR-2000; 2000WO-US007521.  
 PF  
 XX 22-MAR-1999; 99US-0125683P.  
 PR 26-MAR-1999; 99US-0126522P.  
 PR 20-MAY-1999; 99US-0135169P.  
 PR 06-AUG-1999; 99US-0147383P.  
 XX  
 XX (NIJ/) NI J.  
 PA (ROSE/) ROSEN C A.  
 PA (GENTZ/) GENTZ R L.  
 XX  
 XX Ni J, Rosen CA, Gentz RL;  
 XX  
 XX WPI; 2000-594519/56.  
 DR  
 XX  
 XX Nucleic acid molecule encoding a human tumor necrosis factor receptor 2  
 PT and its two splice variants, useful for treating arthritis or  
 PT inflammation, cancer (such as follicular lymphomas) and immunodeficiency  
 PT disorders.  
 XX  
 XX Disclosure; Fig 16; 373pp; English.  
 PS  
 XX This invention relates to an isolated nucleic acid molecule encoding a  
 CC human tumour necrosis factor (TNF)-receptor related protein TR2. Included  
 CC in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.  
 CC The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a  
 CC member of the TNFR superfamily. The invention includes a method for the  
 CC treatment of arthritis or inflammation using an antibody directed against  
 CC a fragment of the TR2 protein. TR2 is agonists, antagonists and  
 CC antibodies exhibit cytostatic, dermatological, antianemic,  
 CC immunosuppressive, anti-allergic, antiarthritic, antiparkinsonian, and  
 CC antiinflammatory, neuroprotective, neurotropic, antiparkinsonian, and  
 CC cerebroprotective activity. The methods are useful for treating arthritis  
 CC or inflammation, cancer (such as follicular lymphomas, carcinoma with p53  
 CC mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an  
 CC immunodeficiency or for enhancing an in vivo leukocyte response to an  
 CC antigen. Anti-TR2 antibodies are useful for treating, inhibiting or  
 CC preventing autoimmune diseases (such as autoimmune haemolytic anaemia,  
 CC dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and  
 CC inflammatory myopathies) and immunodeficiency disorders (such as severely  
 CC combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative  
 CC disorder, or Nezelof syndrome-combined immunodeficiency with IgA). TR2,  
 CC TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or  
 CC antagonists are useful for treating or preventing autoimmune diseases and  
 CC inhibit the growth, progression and/or metastasis of cancers. They are  
 CC also used to activate, differentiate or proliferate cancerous cells or  
 CC tissues, and can be used to treat diseases associated with increased cell  
 CC survival, or the inhibition of apoptosis, e.g. Alzheimer's disease,  
 CC Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful  
 CC as sources for generating antibodies, as molecular weight markers. This  
 CC sequence represents the tumour necrosis factor receptor (TNFR) domain of  
 CC the human 4-1BB protein. The sequence was used in the characterisation of  
 CC the TR2 receptor protein of the invention  
 XX  
 XX Sequence 132 AA;  
 Query Match 82.7%; Score 115; DB 3; Length 132;  
 Best Local Similarity 80.0%; Pred. No. 2.7e-09;



XX DT 23-APR-1999 (first entry)

XX DE Human h4-1BBSV receptor protein variant.

XX XX

KW h4-1BBSV receptor; human, splice variant; antagonist; treatment;

KW disease prevention; endotoxic shock; inflammation; cerebral malaria;

KW HIV virus activation; graft rejection; bone resorption; cachexia;

KW gene therapy.

XX XX

OS Homo sapiens.

OS Synthetic.

XX XX

XX Key Location/Qualifiers

FT Misc-difference 33..34

FT /note= "Site of deletion of residues GTFCDNRNQCSPC

FT PPNSSAGGQRTCDICQCK corresponding to amino acid

FT residues 34-69 of the wild-type protein"

XX XX

XX US5874240-A.

XX PN 23-FEB-1999.

XX XX

XX PF 13-MAR-1997; 97US-00816605.

XX PR 15-MAR-1996; 96US-0013474P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Dillon PJ, Yu G, Ni J, Gentz R;

XX XX

DR WPI; 1999-179974/15.

XX XX

PT New nucleic acid encoding human 4-1BB receptor splicing variant - useful

PT in treating h4-1BBSV mediated disease states such as endotoxic shock,

PT inflammation, graft rejection and inactivation of HIV.

XX XX

PS Claim 29; Page; 28pp; English.

XX XX

CC This sequence represents a human h4-1BBSV receptor protein variant which

CC has antagonistic properties. This protein may be used to treat/prevent

CC disease states mediated by h4-1BBSV receptors such as endotoxic shock,

CC inflammation, cerebral malaria, activation of the HIV virus, graft

CC rejection, bone resorption and cachexia. The h4-1BBSV coding sequences

CC are useful in gene therapy. This sequence does not appear in the

CC specification but has been created from the wild-type sequence

CC represented in Fig 2

XX XX

SQ Sequence 219 AA;

Query Match 82.7%; Score 115; DB 2; Length 219;

Best Local Similarity 80.0%; Pred. NO. 5e-09;

Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25

|||||:|||||:|||||:|||||:|||||

Db 97 CRPWTNCSLDGRSVLVNGTKERDVV 121

RESULT 16

AAE08545

ID AAE08545 standard; protein; 219 AA.

XX AC AAE08545;

XX XX

DT 15-NOV-2001 (first entry)

XX XX

DE Human h4-1BB splicing variant (h4-1BBSV) receptor.

XX XX

KW Human; h4-1BB receptor splicing variant; h4-1BBSV; gene therapy; tumour;

KW tumour necrosis factor; TNF; restenosis; cytotoxicity; endotoxic shock;

KW wound healing; autoimmune disease; acquired immunodeficiency syndrome;

KW AIDS; graft-host rejection; cellular proliferation; cerebral malaria;

KW bone resorption; human immunodeficiency virus; HIV; graft rejection;

KW inflammation; antibacterial; immunosuppressive; vulnerary; vasotropic;

KW antiinflammatory; protozoacide; cachexia; immunomodulator; virucide.

XX OS Homo sapiens.

XX XX

XX Key Location/Qualifiers

FT Peptide 1..18

FT /label= Signal\_peptide

FT Protein 19..219

FT /label= Mature\_human\_h4-1BBSV\_receptor

FT Domain 19..150

FT /label= Extracellular\_domain

FT Domain 151..177

FT /label= Transmembrane\_domain

XX XX

PN US2001014465-A1.

XX XX

XX PD 16-AUG-2001.

XX XX

XX PF 19-DEC-2000; 2000US-00739394.

XX XX

XX PR 15-MAR-1996; 96US-0013474P.

XX PR 13-MAR-1997; 97US-00816605.

XX PR 22-FEB-1999; 99US-00253549.

XX XX

XX (NIJG/) NI J.

XX PA (YUGG/) YU G.

XX PA (GENT/) GENTZ R.

XX PA (DILL/) DILLON P J.

XX XX

XX NI J, Yu G, Gentz R, Dillon PJ;

XX XX

XX WPI; 2001-529104/58.

XX DR N-PSDB; AAD15246.

XX XX

PT New human 4-1BB receptor splicing variant polypeptides and

PT polynucleotides, useful for research, diagnosis, prevention and treatment

PT of tumors, cytotoxicity, autoimmune diseases, acquired immunodeficiency

PT syndrome and graft rejection.

XX XX

PS Claim 15; Fig 1; 28pp; English.

XX XX

CC The present invention relates to an isolated human 4-1BB receptor

CC splicing variant (h4-1BBSV, where 4-1BB is a member of tumour necrosis

CC factor (TNF) family of ligands) polypeptide. h4-1BBSV cDNA is used in

CC gene therapy. h4-1BBSV is useful for research, biological, clinical and

CC therapeutic purposes. h4-1BBSV, its fragments, analogues or derivatives

CC are useful as an immunogen to produce antibodies which are useful for

CC isolating and identifying clones expressing the polypeptide or to purify

CC the polypeptide. h4-1BBSV is useful for diagnosis and treatment of

CC disorders of cells, tissues and organisms and its nucleic acid is useful

CC for detecting complementary polynucleotides for e.g. as a diagnostic

CC reagent and for chromosomal identification. h4-1BBSV receptor agonists

CC are useful for preventing, treating tumours, restenosis, cytotoxicity,

CC bacterial and viral infection, deleterious effects of ionising radiation,

CC autoimmune diseases, acquired immunodeficiency syndrome (AIDS) and graft-

CC host rejection, to regulate immune responses, wound healing and cellular

CC proliferation and antagonists are useful for treating and/or preventing

CC endotoxic shock, inflammation, cerebral malaria, activation of human

CC immunodeficiency virus (HIV) virus, bone resorption, graft rejection and

CC cachexia. The present sequence is human h4-1BBSV receptor

XX XX

SQ Sequence 219 AA;

Query Match 82.7%; Score 115; DB 4; Length 219;

Best Local Similarity 80.0%; Pred. NO. 5e-09;

Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25

|||||:|||||:|||||:|||||:|||||

Db 97 CRPWTNCSLDGRSVLVNGTKERDVV 121

RESULT 17  
ABB94639  
ID ABB84639 standard; protein; 219 AA.  
XX  
AC ABB84639;  
XX  
XX  
DT 05-FEB-2003 (first entry)  
XX  
DE Human h4-1BBSV receptor.  
XX  
XX  
KW Human; h4-1BBSV receptor; anti-tumour; virucide; immunosuppressive;  
KW anti-HIV; antibacterial; antiinflammatory; protozoacide; immunomodulator;  
KW vasotropic; gene therapy; chromosome mapping; extracellular domain;  
KW endotoxic shock; cytotoxicity; cerebral malaria; autoimmune disease.  
KW human immunodeficiency virus; HIV; graft-host rejection; bone resorption;  
KW cachexia; tumour; ionizing radiation; acquired immunodeficiency syndrome;  
KW AIDS; endothelial cell; proliferation; haematopoietic cell; restenosis;  
KW autoimmune disease.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..18  
FT Protein /label= leader\_sequence  
FT /label= h4-1BBSV receptor  
FT /note= "region specifically claimed in claim 1b"  
FT Domain 19..219  
FT /label= soluble\_extracellular\_domain  
FT /note= "region specifically claimed in claim 1a"  
FT Domain 151..177  
FT /label= transmembrane\_domain  
XX  
US2002127651-A1.  
XX  
PD 12-SEP-2002.  
XX  
XX 15-MAR-2002; 2002US-00097330.  
XX  
PR 15-MAR-1996; 96US-0013474P.  
PR 13-MAR-1997; 97US-0081660S.  
PR 22-FEB-1999; 99US-00253549.  
PR 19-DEC-2000; 2000US-00739394.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Ni J, Yu G, Gentz RL, Dillon PJ;  
XX  
XX WPI; 2003-066900/06.  
XX  
XX N-PSDB; ABS57520.  
XX  
XX Novel isolated h4-1BBSV receptor polypeptide, useful for treating tumors,  
XX providing resistance to bacteria, viruses and parasites, to induce  
XX proliferation of endothelial cells, and to treat restenosis.  
XX  
XX  
XX Example 2; Fig 1A-B; 29pp; English.  
XX  
XX This invention describes a novel human h4-1BBSV receptor or a sequence  
XX that is at least 85% identical to the h4-1BBSV receptor. The product of  
XX the invention has anti-tumour, virucide, immunosuppressive, anti-HIV,  
XX antibacterial, antiinflammatory, protozoacide, immunomodulator and  
XX vasotropic activity and can be used for gene therapy and chromosome  
XX mapping. h4-1BBSV is useful for diagnosing a disease or susceptibility to  
XX a disease related to underexpression of h4-1BBSV or for identifying  
XX agonists and antagonists. The soluble extracellular domain of h4-1BBSV  
XX receptor polypeptide is useful for treating and/or preventing endotoxic  
XX shock, cytotoxicity, inflammation, cerebral malaria, activation of human  
XX immunodeficiency virus (HIV), graft-host rejection, bone resorption or  
XX cachexia, tumours, autoimmune disease, ionizing radiation, acquired  
XX immunodeficiency syndrome (AIDS), for providing resistance to bacteria,  
XX viruses and parasites, to induce proliferation of endothelial cells and  
XX certain haematopoietic cells, to treat restenosis and to prevent certain

CC autoimmune diseases after stimulation of h4-1BBSV receptor by an agonist.  
CC This sequence represents the human 4-1BBSV receptor described in the  
CC disclosure of the invention  
XX  
SQ Sequence 219 AA;  
Query Match 82.7%; Score 115; DB 6; Length 219;  
Best Local Similarity 80.0%; Pred. No. 5e-09;  
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CRPWTNCSLDGRSVLKTGTTTEKVV 25  
Db 97 CRPWTNCSLDGRSVLVTNGTKERDVV 121  
XX  
XX  
XX AAR74087;  
XX  
XX 21-JAN-1996 (first entry)  
XX  
XX Human receptor induced by lymphocyte activation (ILA).  
DE  
XX  
XX ILA; receptor inducible by lymphocyte activation; disease diagnosis;  
KW antiinflammatory.  
XX  
XX Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..17  
FT /note= "signal peptide"  
FT Misc-difference 138  
FT /note= "potential N-glycosylation site"  
FT Misc-difference 149  
FT /note= "potential N-glycosylation site"  
FT Domain 187..213  
FT /note= "transmembrane domain"  
FT Misc-difference 234  
FT /note= "casein-kinase-II phosphorylation site"  
FT Misc-difference 235  
FT /note= "casein-kinase-II phosphorylation site"  
FT Binding-site 241..244  
FT /note= "potential ligand binding site"  
FT Misc-difference 242  
FT /note= "protein-kinase phosphorylation site"  
XX  
XX CA2108401-A.  
XX  
XX 28-MAR-1995.  
XX  
XX 14-OCT-1993; 93CA-02108401.  
XX  
XX 27-SEP-1993; 93US-00127693.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Lotz M, Schwarz H;  
XX WPI; 1995-194420/26.  
XX N-PSDB; AAR74087.  
XX  
XX New receptor inducible by lymphocyte activation - used to develop prods.  
XX for the diagnosis and treatment of inflammatory host defence pathology.  
XX  
XX Claim 55; Page 61; 91pp; English.  
XX  
XX ILA may be used to identify a host defence inflammatory response in body  
XX tissue. The ILA agents can be used to detect an ILA-mediated pathology  
XX such as atherosclerosis, autoimmune disease (rheumatoid arthritis,  
XX transplant rejection, pathogenic host defense responses to microorganism  
XX and malignancy such as lung carcinoma

```
XX SQ Sequence 255 AA;
Query Match      82.7%; Score 115; DB 2; Length 255;
Best Local Similarity 80.0%; Pred. No. 6e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLVNGTKERDVV 157

RESULT 19
AAR64197
ID AAR64197 standard; protein; 255 AA.
XX AC AAR64197;
XX DT 25-MAR-2003 (revised)
DT 08-AUG-1995 (first entry)
XX DE Human 4-1BB polypeptide.
XX KW T-cell; lymphocyte; activation; tissue culture; clone; cell lines;
KW proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine.
XX OS Homo sapiens.
XX PN WO9426290-A1.
XX PD 24-NOV-1994.
XX PF 06-MAY-1994; 94WO-US005036.
XX PR 07-MAY-1993; 93US-00060843.
XX PA (IMVU ) IMMUNEX CORP.
XX PI Goodwin RG, Smith CA, Alderson MR;
XX WPI; 1995-022265/03.
XX DR N-PSDB; AAQ75424.
XX CY Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor 4-1BB
PT to transduce signal.
XX PS Claim 39; Page 47-48; 65pp; English.
XX CC The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see AAQ75423)
CC are useful in a pharmaceutical composition for stimulating the immune
CC system. The 4-1BB and 4-1BB-L polypeptides are also useful for exploring
CC mechanisms of T-cell activation, as they are expressed on T lymphocytes.
CC 4-1BB-L can be used as a tissue culture reagent for in vitro cultivation
CC of primary T-cells during the derivation of clonal T-cell lines. It may
CC also be used to stimulate proliferation of activated T-cells, used in
CC therapeutic procedures. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 255 AA;

Query Match      82.7%; Score 115; DB 2; Length 255;
Best Local Similarity 80.0%; Pred. No. 6e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLVNGTKERDVV 157

RESULT 20
AAR70977
ID AAR70977 standard; protein; 255 AA.
XX AC AAR70977;
XX DT 25-MAR-2003 (revised)
DT 16-OCT-1995 (first entry)
XX DE H4-1BB receptor protein.
XX KW H4-1BB; receptor protein; immunosuppressive; autoimmune disease;
KW organ transplantation; cell membrane ligand.
XX OS Homo sapiens.
XX PN WO9507984-A1.
XX PD 23-MAR-1995.
XX PF 15-SEP-1994; 94WO-US010457.
XX PR 16-SEP-1993; 93US-00122796.
XX PA (INDV ) UNIV INDIANA FOUND.
XX PI Kwon BS;
XX WPI; 1995-131352/17.
XX DR N-PSDB; AAQ86126.
XX PT Novel cDNA encoding human receptor protein H4-1BB - useful to produce the
PT protein which is used to treat auto-immune disease and facilitate organ
PT transplantation.
XX PS Claim 6; Fig 2; 36pp; English.
XX CC Human peripheral blood lymphocyte-derived cDNA was amplified by PCR using
CC probes based on the mouse receptor protein 4-1BB gene. The PCR product
CC was used to screen a cDNA library of activated human T-cells. The
CC isolated cDNA (AAQ86126), deposited as NRRL AAB21131, encoded the human
CC homolog, H4-1BB (AAR70977), of 4-1BB. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX SQ Sequence 255 AA;

Query Match      82.7%; Score 115; DB 2; Length 255;
Best Local Similarity 80.0%; Pred. No. 6e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLVNGTKERDVV 157

RESULT 21
AAW26658
ID AAW26658 standard; protein; 255 AA.
XX AC AAW26658;
XX DT 25-MAR-2003 (revised)
DT 25-FEB-1998 (first entry)
XX DE Human 4-1BB receptor.
XX KW 4-1BB ligand; 4-1BB-L; receptor; human; cytokine; T lymphocyte; T cell;
KW proliferation; immunostimulant.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FH Peptide 1..23
FH Domain 24..186
FH Modified-site 115..117
FH /note= "Asn is N-glycosylated"
```



```

FT Modified-site 126..128
FT /note= "Asn is N-glycosylated"
FT Domain 187..213
FT /label= Transmembrane
FT Domain 214..255
FT /label= Extracellular
XX
XX US5674704-A.
XX
XX 07-OCT-1997.
XX
XX 06-MAY-1994; 94US-00236918.
XX
XX 07-MAY-1993; 93US-00060843.
XX
XX (IMVU ) IMMUNEX CORP.
XX
XX Alderson MR, Goodwin RG, Smith CA;
XX
XX WPI; 1997-502333/46.
XX N-PSDB; AAT91026.
XX
XX DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating T-cell
XX proliferation in vitro, and as research tools.
XX
XX Example 2; Col 43-44; 32pp; English.
XX
XX This protein comprises human 4-1BB, a member of the tumour necrosis
XX factor receptor superfamily that is expressed on cells that include, but
XX are not limited to, stimulated human peripheral blood lymphocytes. Its
XX amino acid sequence was deduced from an isolated cDNA clone (see
XX AAT91026) obtained from human peripheral blood T-lymphocytes. A novel
XX claimed cytokine, designated 4-1BB ligand (4-1BB-L) has been identified,
XX cloned and sequenced (see AAW26657) that binds to 4-1BB. 4-1BB-L,
XX especially, its soluble extracellular domain, can be used to stimulate T-
XX cell proliferation in vitro, as a research tool and as an affinity ligand
XX for purifying 4-1BB. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX SQ Sequence 255 AA;

Query Match 82.7%; Score 115; DB 2; Length 255;
Best Local Similarity 80.0%; Pred. No. 6e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
DB 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 22
AAAY28688
ID AAY28688 standard; protein; 255 AA.
XX
XX AAY28688;
XX
XX 13-OCT-1999 (first entry)
XX
XX Human receptor protein 4-1BB.
XX
XX Human receptor protein 4-1BB; H4-1BB; T cell activation; proliferation;
XX mouse 4-1BB cDNA; monoclonal antibody; immune response;
XX organ transplantation; autoimmune disease; diabetes; cancerous tumour;
XX rheumatoid arthritis; lupus; nerve growth factor receptor.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Protein 18..255
XX /note= "Purified human 4-1BB"
XX
XX WO9936093-A1.
XX
XX 22-JUL-1999.

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XX 14-JAN-1999; 99WO-US000823.
XX
XX 14-JAN-1998; 98US-00007097.
XX
XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX (KWON/) KWON B S.
XX
XX Kwon BS;
XX
XX WPI; 1999-444325/37.
XX N-PSDB; AAZ08961.
XX
XX Using human receptor protein 4-1BB ligands to, e.g. treat Diabetes
XX Mellitus, Rheumatoid Arthritis and Systemic Lupus Erythematosus.
XX
XX Claim 4; Page 77-78; 86pp; English.
XX
XX The present sequence is a human receptor protein 4-1BB. 4-1BB is
XX structurally related to members of the nerve growth factor receptor. It
XX contains a putative zinc finger structure similar to that of yeast eIF-2b
XX protein. Probes derived from mouse 4-1BB cDNA are used to isolate cDNA of
XX H4-1BB. The H4-1BB protein, its ligands, and various monoclonal
XX antibodies have therapeutic uses. They may be used to enhance or suppress
XX T cell activation and proliferation; B cell proliferation; treating
XX cancerous tumours and AIDS. The use of H4-1BB to block H4-1BB ligand
XX binding has practical application in the suppression of immune system
XX during organ transplantation or against autoimmune diseases including
XX diabetes, rheumatoid arthritis, and lupus
XX
XX SQ Sequence 255 AA;

Query Match 82.7%; Score 115; DB 2; Length 255;
Best Local Similarity 80.0%; Pred. No. 6e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
DB 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 23
AAAY33214
ID AAY33214 standard; protein; 255 AA.
XX
XX AAY33214;
XX
XX 18-NOV-1999 (first entry)
XX
XX Human CD137 protein.
XX
XX CD137; monocyte growth factor; proliferation; peripheral monocyte;
XX treatment; disease; antitumor; antibacterial; antiviral; antifungal;
XX immunostimulatory; non-specific immune response; phagocytosis;
XX intracellular destruction; microorganism; immune complex; antibody;
XX cytotoxicity; tumor cell; macrophage; hematopoietic system; leucopenia;
XX chemotherapy; radiation; therapy; wound healing disorder; tumor; fungal;
XX bacterial; viral infection; immunosuppressant; gene therapy; human.
XX
XX Homo sapiens.
XX
XX WO9944629-A2.
XX
XX 10-SEP-1999.
XX
XX 05-MAR-1999; 99WO-EP001440.
XX
XX 05-MAR-1998; 98EP-00103859.
XX
XX (MERC ) MERCKLE GMBH.
XX
XX Schwarz H, Langstein J;
XX

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DR WPI: 1999-550983/46.  
DR N-PSDB; AA059769.  
XX  
PT Use of monocyte growth factor CD137 for stimulating proliferation of  
PT peripheral monocytes, particularly for treating immune deficiency, e.g.  
PT following cancer therapy.  
XX  
XX  
PS Claim 12; Fig 1A; 57pp; German.  
XX  
CC This invention describes a novel use of the human monocyte growth factor  
CC CD137, or its functional analogs, for (i) stimulating proliferation of  
CC peripheral monocytes; and (ii) treating diseases that are associated with  
CC disorders of a cellular system that includes monocytes (and/or their  
CC derived cells, precursor or progenitors) or where the origin and/or  
CC progression is treatable by stimulating proliferation of such cells. The  
CC products of the invention have antitumor, antibacterial, antiviral,  
CC antifungal and immunostimulatory activity. Stimulating proliferation of  
CC monocytes promotes the non-specific immune response, i.e. it increases  
CC phagocytosis and intracellular destruction of microorganisms, immune  
CC complexes and damaged cells, and improves antibody (in)dependent  
CC cytotoxicity to tumor cells. CD137 is used, in vivo or ex vivo, to treat  
CC diseases associated with a defective immune response where caused by  
CC inadequate numbers of active monocytes/macrophages, especially damage to  
CC the hematopoietic system (leucopenia) caused by chemotherapy or radiation  
CC therapy; disorders of wound healing (e.g. in dialysis or diabetic  
CC patients, or those with chronic venous insufficiency); tumors; bacterial,  
CC fungal or viral infections; (non-)congenital or (non-)inherited diseases  
CC or injury to the immune system; injury induced by treatment with  
CC immunosuppressants (e.g. patients with chronic arthritis or autoimmune  
CC disease, or transplant patients). Nucleic acid encoding (i) can be used  
CC similarly, in gene therapy procedures. Proliferation of peripheral  
CC monocytes is achieved independently of hematopoietic stem cells. This  
CC sequence represents the human CD137 protein described in the method of  
CC the invention  
XX  
XX  
SQ Sequence 255 AA;  
Query Match 82.7%; Score 115; DB 2; Length 255;  
Best Local Similarity 80.0%; Pred. No. 6e-09;  
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CRPWTNCSLDGSRVLKGTGTERDGV 25  
DB 133 CRPWTNCSLDGSKVLVNGTKERDGV 157  
RESULT 24  
AAE08546  
ID AAE08546 standard; protein; 255 AA.  
XX  
AC AAE08546;  
XX  
XX  
DT 15-NOV-2001 (first entry)  
XX  
DE Human h4-1BB receptor.  
XX  
KW Human; h4-1BB receptor splicing variant; h4-1BSV; gene therapy; tumour;  
KW tumour necrosis factor; TNF; restenosis; cytotoxicity; endotoxin shock;  
KW wound healing; autoimmune disease; acquired immunodeficiency syndrome;  
KW AIDS; graft-host rejection; cellular proliferation; cerebral malaria;  
KW bone resorption; human immunodeficiency virus; HIV; graft rejection;  
KW inflammation; antibacterial; immunosuppressive; vulvulnary; vasotropic;  
KW antinflammatory; protozoacide; cachexia; immunomodulator; virucide.  
XX  
OS Homo sapiens.  
XX  
XX US2001014465-A1.  
PN 19-DEC-2000; 2000US-00739394.  
XX  
PD 16-AUG-2001.  
XX  
PF 19-DEC-2000; 2000US-00739394.  
XX  
XX 15-MAR-1996; 96US-0013474P.  
PR

PR 13-MAR-1997; 97US-00816605.  
PR 22-FEB-1999; 99US-00253549.  
XX  
PA (NIJJ/) NI J.  
PA (YUGG/) YU G.  
PA (GENT/) GENTZ R.  
PA (DILL/) DILLON P J.  
XX  
PI Ni J, Yu G, Gentz R, Dillon PJ;  
XX  
DR WPI: 2001-529104/58.  
XX  
PT New human 4-1BB receptor splicing variant polypeptides and  
PT polynucleotides, useful for research, diagnosis, prevention and treatment  
PT of tumors, cytotoxicity, autoimmune diseases, acquired immunodeficiency  
PT syndrome and graft rejection.  
XX  
XX Disclosure; Fig 2; 28pp; English.  
XX  
CC The present invention relates to an isolated human 4-1BB receptor  
CC splicing variant (h4-1BSV, where 4-1BB is a member of tumour necrosis  
CC factor (TNF) family of ligands) polypeptide. h4-1BSV CDNA is used in  
CC gene therapy. h4-1BSV is useful for research, biological, clinical and  
CC therapeutic purposes. h4-1BSV, its fragments, analogues or derivatives  
CC are useful as an immunogen to produce antibodies which are useful for  
CC isolating and identifying clones expressing the polypeptide or to purify  
CC the polypeptide. h4-1BSV is useful for diagnosis and treatment of  
CC disorders of cells, tissues and organisms and its nucleic acid is useful  
CC for detecting complementary polynucleotides for e.g. as a diagnostic  
CC reagent and for chromosomal identification. h4-1BSV receptor agonists  
CC are useful for preventing, treating tumours, restenosis, cytotoxicity,  
CC bacterial and viral infection, deleterious effects of ionising radiation,  
CC autoimmune diseases, acquired immunodeficiency syndrome (AIDS) and graft-  
CC host rejection, to regulate immune responses, wound healing and cellular  
CC proliferation and antagonists are useful for treating and/or preventing  
CC endotoxin shock, inflammation, cerebral malaria, activation of human  
CC immunodeficiency virus (HIV) virus, bone resorption, graft rejection and  
CC cachexia. The present sequence is human h4-1BB receptor  
XX  
XX  
SQ Sequence 255 AA;  
Query Match 82.7%; Score 115; DB 4; Length 255;  
Best Local Similarity 80.0%; Pred. No. 6e-09;  
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CRPWTNCSLDGSRVLKGTGTERDGV 25  
DB 133 CRPWTNCSLDGSKVLVNGTKERDGV 157  
RESULT 25  
AAE05021  
ID AAE05021 standard; protein; 255 AA.  
XX  
AC AAE05021;  
XX  
XX  
DT 15-MAR-2001 (first entry)  
XX  
DE Human tumour necrosis factor receptor 4-1BB protein SEQ ID NO:11.  
XX  
KW Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nototropic;  
KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;  
KW tumour necrosis factor related apoptosis inducing ligand; vasotropic;  
KW immunosuppressive; neuroprotective; antiviral; antinflammatory;  
KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;  
KW gene therapy; restenosis; graft versus host disease; tumour; cancer;  
KW apoptotic cell death related disease; autoimmune disorder;  
KW cardiovascular disorder; viral infection.  
XX  
OS Homo sapiens.  
XX  
XX WO200071150-A1.  
PN

PD 30-NOV-2000.  
XX  
PF 18-MAY-2000; 2000MO-US013515.  
PR  
XX 20-MAY-1999; 99US-0135164P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Wei Y, Ruben SM, Gentz RL, Ni J;  
XX WPI; 2001-041051/05.  
XX  
XX Nucleic acid encoding a TRID polypeptide, also referred to as tumor  
PT necrosis factor receptor 5, useful in the diagnosis, treatment or  
PT prevention of cancer, autoimmune disorders and viral infection.  
XX  
PS Disclosure; Fig 2; 285pp; English.  
XX  
XX The present invention describes the human TRID protein (tumour necrosis  
CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without  
CC intracellular domain, also referred to as tumour necrosis factor receptor  
CC 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, neutrotropic,  
CC neuroprotective, antiviral, anti-inflammatory, anticonvulsant,  
CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic  
CC activities, and can be used in gene therapy. The TRID polynucleotides are  
CC useful for detecting complementary polynucleotides. TRID proteins and  
CC polynucleotides are useful in the treatment of tumours, resistance to  
CC parasite, bacteria and viruses, restenosis and graft versus host disease.  
CC They are also useful for inducing proliferation of T-cells, endothelial  
CC cells and certain haematopoietic cells, to regulate antiviral responses  
CC and to prevent certain autoimmune diseases after stimulation of TRID by  
CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID  
CC associated with increased or decreased apoptotic cell death. The TRID  
CC polynucleotides, proteins, antibodies, agonists and antagonists are  
CC useful in the diagnosis, treatment or prevention of: (a) cancer; (b)  
CC autoimmune disorders; (c) diseases associated with increased apoptosis;  
CC (d) cardiovascular disorders; and (e) viral infection. The present  
CC sequence represents a tumour necrosis factor receptor used in comparison  
CC with TRID in the exemplification of the present invention  
XX  
SQ Sequence 255 AA;  
Query Match 82.7%; Score 115; DB 4; Length 255;  
Best Local Similarity 80.0%; Pred. No. 6e-09;  
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CRPWTNCSLDGRSVLKTGTETKDVV 25  
DB 133 CRPWTNCSLDGRSVLKTGTETKDVV 157  
RESULT 26  
ABB75955  
ID ABB75955 standard; protein; 255 AA.  
XX AC ABB75955;  
XX  
DT 12-JUL-2002 (first entry)  
DE Human cytokine receptor 4-1BB.  
XX Cytokine; receptor; 4-1BB; human.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT Peptide 1..23  
FT /label= Signal\_peptide  
FT Protein 24..255  
FT /label= Mature\_protein  
FT Domain 24..186  
FT /note= "extracellular domain"

FT Modified-site 138..140  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 149..151  
FT /note= "Asn is N-glycosylated"  
FT Region 186..213  
FT /note= "transmembrane region"  
FT Domain 214..255  
FT /note= "cytoplasmic domain"  
XX  
PN US6355779-B1.  
XX  
PD 12-MAR-2002.  
XX  
XX 10-SEP-1998; 98US-00150864.  
PF  
XX 07-MAY-1993; 93US-00060843.  
PR 06-MAY-1994; 94US-00236918.  
PR 05-AUG-1997; 97US-00910449.  
XX (IMMV ) IMMUNEX CORP.  
PA Goodwin RG, Smith CA, Alderson MR;  
XX N-PSDB; ABL54048.  
XX WPI; 2002-380940/41.  
XX N-PSDB; ABL54048.  
XX New antibody specific for the cytokine 4-1BB-ligand, useful for  
PT immunoaffinity purification of the ligand.  
XX  
XX Example 2; Col 43-44; 3lpp; English.  
XX  
XX The present sequence is the protein sequence of the human cytokine  
CC receptor, 4-1BB. The sequence was deduced from a cDNA clone (see  
CC ABL54048) obtained from a human peripheral blood T-lymphocyte cDNA  
CC library. It shows 60% identity to murine 4-1BB (see ABB75954). A portion  
CC of the extracellular (ligand binding) domain of the human 4-1BB cytokine  
CC receptor was utilised in a human 4-1BB/human IgG1 Fc fusion protein,  
CC which was used to identify the human 4-1BB ligand (4-1BB-L, see  
CC ABB75953). The invention provides novel murine and human 4-1BB-L  
CC polypeptides and human 4-1BB polypeptides, as well as DNA sequences  
CC encoding them, recombinant expression vectors and host cells, and methods  
CC for producing the novel polypeptides by culturing the transformed host  
CC cells. Soluble forms of the 4-1BB-L and 4-1BB polypeptides, derived from  
CC their extracellular domains, have therapeutic value. Antibodies that are  
CC immunoreactive with 4-1BB-L or human 4-1BB are claimed  
XX  
SQ Sequence 255 AA;  
Query Match 82.7%; Score 115; DB 5; Length 255;  
Best Local Similarity 80.0%; Pred. No. 6e-09;  
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CRPWTNCSLDGRSVLKTGTETKDVV 25  
DB 133 CRPWTNCSLDGRSVLKTGTETKDVV 157  
RESULT 27  
ABB39863  
ID ABB39863 standard; protein; 255 AA.  
XX AC ABB39863;  
XX  
DT 11-AUG-2003 (first entry)  
DE Human MOCEPTIN polypeptide.  
XX  
XX MOCEPTIN; tumour necrosis factor receptor; TNF receptor; anorectic;  
KW antilipemic; antiarteriosclerotic; antidiabetic; cerebroprotective;  
KW hypotensive; immunomodulator; antidepressant; human; receptor.  
XX  
XX Homo sapiens.  
XX

FH Key Location/Qualifiers  
 FT Peptide 1..17  
 FT Protein /note= "putative signal peptide"  
 FT Protein 18..255  
 FT Domain /note= "mature protein"  
 FT Domain 18..186  
 FT Domain /note= "extracellular domain"  
 FT Domain 187..213  
 FT Domain /note= "transmembrane domain"  
 FT Domain 214..255  
 FT Domain /note= "intracellular domain"  
 XX WO2003011325-A1.  
 XX  
 XX PD 13-FEB-2003.  
 XX  
 XX PF 25-JUL-2002; 2002WO-IB003499.  
 XX  
 XX PR 27-JUL-2001; 2001US-0308142P.  
 XX  
 XX (GEST ) GENSET SA.  
 XX  
 XX PI Lucas J, Dialynas D, Briggs K;  
 XX  
 XX WI 2003-268084/26.  
 XX N-PSDB; ACC47324.  
 XX  
 XX PT New agonist and antagonist of MOCEPTIN (a member of the Tumor Necrosis  
 PT Factor Receptor family) activity, useful for preventing or treating  
 PT obesity-related diseases (e.g. hyperlipidemia or stroke), or increasing  
 PT body mass.  
 XX  
 XX PS Disclosure; Page 32-33; 37pp; English.  
 XX  
 XX CC The invention relates to an agonist or antagonist of MOCEPTIN (a member  
 CC of the Tumour Necrosis Factor Receptor family) activity. The antagonist  
 CC or agonist of MOCEPTIN activity, or the composition comprising the  
 CC agonist or antagonist, is useful for preventing or treating an obesity-  
 CC related disorder or disease in an individual. In particular, the agonist  
 CC of MOCEPTIN activity is useful for treating or preventing obesity-related  
 CC diseases, e.g. hyperlipidemia, atherosclerosis, insulin resistance,  
 CC diabetes, stroke or hypertension. The agonist is also useful for reducing  
 CC body mass and maintaining weight loss. The antagonist of MOCEPTIN  
 CC activity is useful for increasing body mass, or for treating or  
 CC preventing disorders associated with excessive weight loss, e.g.  
 CC cachexia, cancer-related weight loss, AIDS-related weight loss, chronic  
 CC inflammatory disease-related weight loss, or anorexia. The present  
 CC sequence represents a human MOCEPTIN polypeptide  
 XX  
 XX SQ Sequence' 255 AA;  
 Query Match 82.7%; Score 115; DB 6; Length 255;  
 Best Local Similarity 80.0%; Pred. No. 6e-09;  
 Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
 DB 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157  
 RESULT 28  
 ID ABB84640 standard; protein; 255 AA.  
 XX  
 XX AC ABB84640;  
 XX  
 XX DT 05-FEB-2003 (first entry)  
 XX  
 XX DE Human h4-1BB receptor.  
 XX  
 XX KW Human; h4-1BBSV receptor; anti-tumour; virucide; immunosuppressive;  
 KW anti-HIV; antibacterial; antiinflammatory; protozoacide; immunomodulator;  
 KW vasotropic; gene therapy; chromosome mapping; extracellular domain;

KW endotoxigen shock; cytotoxicity; cerebral malaria; autoimmune disease;  
 KW human immunodeficiency virus; HIV; graft-host rejection; bone resorption;  
 KW cachexia; tumour; ionizing radiation; acquired immunodeficiency syndrome;  
 KW AIDS; endothelial cell; proliferation; haematopoietic cell; restenosis;  
 KW autoimmune disease; h4-1BB.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX PN US2002127651-A1.  
 XX  
 XX PD 12-SEP-2002.  
 XX  
 XX PF 15-MAR-2002; 2002US-00097330.  
 XX  
 XX PR 15-MAR-1996; 96US-0013474P.  
 PR 13-MAR-1997; 97US-00816605.  
 PR 22-FEB-1999; 99US-00253549.  
 PR 19-DEC-2000; 2000US-00739394.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX PI Ni J, Yu G, Gentz RL, Dillon PJ;  
 XX  
 XX WI 2003-066900/06.  
 XX  
 XX PT Novel isolated h4-1BBSV receptor polypeptide, useful for treating tumors,  
 PT providing resistance to bacteria, viruses and parasites, to induce  
 PT proliferation of endothelial cells, and to treat restenosis.  
 XX  
 XX PS Disclosure; Fig 2; 29pp; English.  
 XX  
 XX CC This invention describes a novel human h4-1BBSV receptor or a sequence  
 CC that is at least 85% identical to the h4-1BBSV receptor. The product of  
 CC the invention has anti-tumour, virucide, immunosuppressive, anti-HIV,  
 CC antibacterial, antiinflammatory, protozoacide, immunomodulator and  
 CC vasotropic activity and can be used for gene therapy and chromosome  
 CC mapping. h4-1BBSV is useful for diagnosing a disease or susceptibility to  
 CC a disease related to underexpression of h4-1BBSV or for identifying  
 CC agonists and antagonists. The soluble extracellular domain of h4-1BBSV  
 CC receptor polypeptide is useful for treating and/or preventing endotox-  
 CC shock, cytotoxicity, inflammation, cerebral malaria, activation of human  
 CC immunodeficiency virus (HIV), graft-host rejection, bone resorption or  
 CC cachexia, tumours, autoimmune disease, ionizing radiation, acquired  
 CC immunodeficiency syndrome (AIDS), for providing resistance to bacteria,  
 CC viruses and parasites, to induce proliferation of endothelial cells and  
 CC certain haematopoietic cells, to treat restenosis and to prevent certain  
 CC autoimmune diseases after stimulation of h4-1BBSV receptor by an agonist.  
 CC This sequence represents the human h4-1BB receptor described in the  
 CC disclosure of the invention  
 XX  
 XX SQ Sequence 255 AA;  
 Query Match 82.7%; Score 115; DB 6; Length 255;  
 Best Local Similarity 80.0%; Pred. No. 6e-09;  
 Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
 DB 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157  
 RESULT 29  
 ID AAE39531 standard; protein; 255 AA.  
 XX  
 XX AC AAE39531;  
 XX  
 XX DT 18-DEC-2003 (first entry)  
 XX  
 XX DE Human protein SEQ ID NO: 2.  
 XX  
 XX KW Human; adhesive; packaging.  
 XX



CC comprising a binding domain polypeptide that is fused to an  
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain  
CC CH2 constant region polypeptide that is fused to the hinge region  
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region  
CC polypeptide that is fused to the CH2 constant region polypeptide. The  
CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin  
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge  
CC region polypeptide, derived from (a) having 3 or more cysteine residues;  
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide  
CC contains 2 cysteine residues, where the first cysteine is not mutated; a  
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from  
CC (a) having 3 or more cysteine residues, where the mutated human IgG1  
CC immunoglobulin hinge region polypeptide contains no more than one  
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region  
CC polypeptide, derived from (a) having 3 or more cysteine residues; where  
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains  
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is  
CC capable of at least one immunological activity comprising antibody  
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The  
CC binding domain polypeptide is capable of specifically binding to an  
CC antigen. Also included are an isolated polynucleotide encoding the  
CC binding domain-immunoglobulin fusion protein, a recombinant expression  
CC construct comprising the polynucleotide (operably linked to a promoter),  
CC a host cell transformed or transfected with a recombinant expression  
CC construct, producing the binding domain-immunoglobulin fusion protein, a  
CC pharmaceutical composition comprising the binding domain-immunoglobulin  
CC fusion protein or polynucleotide and a carrier, and treating a subject  
CC having or suspected of having a malignant condition or a B-cell disorder.  
CC The binding domain-immunoglobulin fusion protein is useful for treating a  
CC subject having or suspected of having a malignant condition or a B-cell  
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,  
CC myelodysplasia, Grave's disease, type 1 diabetes mellitus, multiple  
CC sclerosis or autoimmune disease. The present sequence is a binding domain  
CC -immunoglobulin fusion protein-associated protein sequence. Note: The  
CC sequence data for this patent formed part of the printed specification  
CC and is also available in electronic format directly from USPTO at  
CC [seqdata.uspto.gov/sequence.html?docID=20030118592](http://seqdata.uspto.gov/sequence.html?docID=20030118592). The authors have not  
CC identified the sequences in the printed specification by their SEQ ID  
CC number therefore none of the sequences can be explicitly identified.

XX SQ Sequence 255 AA;  
Query Match 82.7%; Score 115; DB 7; Length 255;  
Best Local Similarity 80.0%; Pred. No. 6e-09; Indels 0; Gaps 0;  
Matches 20; Conservative 2; Mismatches 3;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
DB 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 32  
ADE87541  
ID ADE87541 standard; protein; 255 AA.

AC ADE87541;  
XX  
DT 29-JAN-2004 (first entry)

DE Unknown human receptor H4-1BB.

XX immunosuppressive; H4-1BB ligand binding blocker; human;  
KW receptor protein; H4-1BB; B-cell proliferation stimulator;  
KW T-cell proliferation enhancer; immune system suppressor; transplantation;  
KW autoimmune disease.

XX Homo sapiens.

XX US2003082157-A1.

XX 01-MAY-2003.

XX 12-JUN-2002; 2002US-00170997.

XX 07-NOV-1988; 88US-00267577.  
PR 30-JUL-1992; 92US-00322896.  
PR 01-FEB-1993; 93US-00012269.  
PR 05-JUN-1995; 95US-00460976.  
PR 22-OCT-1997; 97US-00955573.  
XX (KWON/) KWON B S.  
XX  
XX Kwon BS;  
XX WPI; 2003-576599/54.  
DR N-PSDB; ADE87540.  
XX  
XX New cDNA, or its encoded receptor protein H4-1BB, useful as probes to  
PT isolate DNAs or ligands to the receptor protein H4-1BB, or for blocking  
PT H4-1BB ligand binding to facilitate organ transplantation or treat  
PT autoimmune diseases.  
XX  
XX Disclosure; SEQ ID NO 2; 19pp; English.

XX The invention describes a cDNA, which encodes for human receptor protein  
CC H4-1BB. The cDNA, or its fragments or derivatives, are useful as a probe  
CC to isolate DNA sequences encoding for proteins similar to the receptor  
CC protein H4-1BB. The receptor protein H4-1BB, or its fragments or  
CC derivatives, is useful as a probe for identifying ligands to the receptor  
CC protein H4-1BB, or for stimulating the proliferation of B-cells  
CC expressing H4-1BB ligands. The monoclonal antibodies against H4-1BB are  
CC useful for enhancing T-cell proliferation of activation. The cDNA or  
CC receptor protein H4-1BB is also useful for blocking H4-1BB ligand  
CC binding, which is particularly useful for suppressing the immune system  
CC during transplantation, or for treating autoimmune diseases. This is the  
CC amino acid sequence of unknown human receptor H4-1BB.

XX SQ Sequence 255 AA;

Query Match 82.7%; Score 115; DB 7; Length 255;  
Best Local Similarity 80.0%; Pred. No. 6e-09; Indels 0; Gaps 0;  
Matches 20; Conservative 2; Mismatches 3;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
DB 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 33  
AAW04174  
ID AAW04174 standard; protein; 255 AA.

AC AAW04174;

DT 12-DEC-1996 (first entry)

XX Human receptor H4-1BB.

XX Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;  
KW B-lymphocyte; B-cell; immunostimulant; cancer; autoimmune disease;  
KW graft rejection; therapy.

XX Homo sapiens.

XX WO9629348-A1.

XX 26-SEP-1996.

XX 22-MAR-1996; 96WO-US003965.

XX 23-MAR-1995; 95US-00409851.

XX (INDV ) UNIV INDIANA FOUND.

XX Kwon BS, Kang C;

DR WPI; 1996-443138/44.  
 DR N-PSDB; AAT39546.  
 XX  
 PT Monoclonal antibody specific for human receptor protein 4-1BB - used to  
 PT enhance proliferation and activation of T-cells for treatment of cancer  
 PT and to inhibit specific ligand binding for treating auto-immune diseases.  
 XX  
 PS Disclosure; Page 36-37; 48pp; English.  
 XX  
 CC Novel human receptor protein H4-1BB (AAW04174) has the potential to  
 CC function as an accessory signaling molecule during T-cell activation and  
 CC proliferation. Its amino acid sequence was deduced from a cDNA clone  
 CC (AAT39546) isolated from activated human T-lymphocytes. Recombinant H4-  
 CC 1BB can be produced in transfected host cells. It is used to isolate  
 CC receptor ligands, to stimulate B-cells expressing such ligands and to  
 CC block H4-1BB ligand binding. A fusion protein of H4-1BB with human  
 CC placental alkaline phosphatase can be used to modify immune responses. A  
 CC monoclonal antibody raised against an immunopeptide (see also AAW04172)  
 CC of H4-1BB is useful in the treatment of cancer and autoimmune diseases  
 XX  
 SQ Sequence 255 AA;  
 Query Match 73.4%; Score 102; DB 2; Length 255;  
 Best Local Similarity 76.0%; Pred. No. 5.5e-07;  
 Matches 19; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 CREWTNCSLDGRSVLTKGTGTEKDVV 25  
 DB 133 CREWTNCSLDGRSVLTKGTGTEKDVV 157  
 RESULT 34  
 AAY59508  
 ID AAY59508 standard; protein; 201 AA.  
 XX  
 AC AAY59508;  
 XX  
 DT 31-MAR-2000 (first entry)  
 XX  
 DE OBM binding protein sequence.  
 XX  
 KW OBM-BP; OBM binding protein; osteoclast formation promoting factor;  
 KW bone metabolic disease; osteoporosis; therapy.  
 XX  
 OS Mus sp.  
 XX  
 PN JPL1332581-A.  
 XX  
 PD 07-DEC-1999.  
 XX  
 PF 20-OCT-1998; 98JP-00316973.  
 XX  
 PR 24-MAR-1998; 98JP-00076232.  
 XX  
 PA (SNOW ) SNOW BRAND MILK PROD CO LTD.  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 DR WPI; 2000-091362/08.  
 DR N-PSDB; AAZ49022.  
 XX  
 PT A new protein, a DNA and its application.  
 XX  
 PS Claim 1; Page 17-18; 18pp; Japanese.  
 XX  
 CC This sequence is the osteoclast formation promoting factor (OBM) binding  
 CC protein (OBM-BP) of the invention. The protein is useful as a preventive  
 CC and/or treating agent for bone metabolic diseases such as osteoporosis.  
 CC Substances which inhibit the binding of OBM to OBM-BP can be used as  
 CC biochemical reagents  
 XX  
 SQ Sequence 201 AA;  
 Query Match 61.9%; Score 86; DB 3; Length 201;

Best Local Similarity 60.0%; Pred. No. 0.00011;  
 Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 CRPWTNCSLDGRSVLTKGTGTEKDVV 25  
 DB 170 CRPWTNCSLDGRSVLTKGTGTEKDVV 194  
 RESULT 35  
 ADE17000  
 ID ADE17000 standard; protein; 443 AA.  
 XX  
 AC ADE17000;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Murine RANK/ human Fc fusion protein with native RANK leader sequence.  
 XX  
 KW RANKL; RANK; receptor activator of nuclear factor-kappa B; ligand;  
 KW cytokine; immunoregulatory; TNF; tumour necrosis factor; TRAF;  
 KW TNF receptor associated factor; autoimmunity; inflammatory; vaccine;  
 KW infectious disease; mouse; chimeric; IgG; immunoglobulin G; mutant;  
 KW murine; murine.  
 XX  
 OS Chimeric.  
 OS Synthetic.  
 OS Mus sp.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..213  
 FT /note= "RANK protein ({seqid:15}) residues 1-213 with  
 FT native leader sequence"  
 FT 214..443  
 FT Region  
 FT /note= "IGF mutein ({seqid:8}) residues 3-232"  
 XX  
 PN US2002086826-A1.  
 XX  
 PD 04-JUL-2002.  
 XX  
 PF 25-MAY-2001; 2001US-00865363.  
 XX  
 PR 23-DEC-1996; 96US-00599782.  
 PR 07-MAR-1997; 97US-0077181P.  
 PR 14-OCT-1997; 97US-0064671P.  
 PR 22-DEC-1997; 97US-00995659.  
 PR 24-MAY-2000; 2000US-00577780.  
 XX  
 PA (IMV ) IMMUNEX CORP.  
 XX  
 PI Anderson DM, Galibert L, Maraskovsky E;  
 XX  
 DR WPI; 2003-605660/57.  
 XX  
 PT Novel RANKL, ligand of receptor activator of nuclear factor-kappa B  
 PT useful for inducing maturation in dendritic cells and enhancing allo-  
 PT stimulatory capacity of dendritic cells.  
 XX  
 PS Example 15; Page; 49pp; English.  
 XX  
 CC This invention relates to a novel isolated RANKL polynucleotide and the  
 CC encoded protein thereof, where RANKL is the ligand of a novel receptor  
 CC referred to as RANK (Receptor Activator of Nuclear factor-Kappa B (NF-  
 CC KB)). Specifically, the invention describes this cytokine receptor/  
 CC ligand pair, and their role in immunoregulatory activity. RANK is a  
 CC member of the TNF (tumour necrosis factor) receptor superfamily and  
 CC shares similarity with CD40, a receptor present on B lymphocytes, and  
 CC associates with TRAFs (TNF receptor associated factors), which are known  
 CC to play an important role in the regulation of the immune and inflammatory  
 CC response. As such, RANK and RANKL can be used in the development of  
 CC diagnostics and therapeutics for use in autoimmune and inflammatory  
 CC diseases. Furthermore, the invention refers to preparing kits that are  
 CC used to detect soluble RANK or RANKL, for screening inhibitors of RANK,

CC for structure-based design of RANKL inhibitors, and in augmenting an  
 CC immune response. It can also be useful as a vaccine adjuvant or a  
 CC therapeutic agent to upregulate an immune response for example in  
 CC infectious disease. This polypeptide sequence is a RANK/ Fc fusion  
 CC protein comprising a soluble form of the murine RANK protein (with native  
 CC leader sequence) fused to a mutant Fc region of human IgG, in an  
 CC exemplification of the invention. NOTE: This sequence is not given in the  
 CC specification but is derived from information provided in example 15.

XX SQ Sequence 443 AA;  
 Query Match 61.9%; Score 86; DB 7; Length 443;  
 Best Local Similarity 60.0%; Pred. No. 0.00029;  
 Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
 Db 170 CRPWTNCTLLGKLEAHQGTTSDDV 194

RESULT 36  
 AAW83200  
 ID AAW83200 standard; protein; 625 AA.  
 XX AC AAW83200;  
 XX DT 11-FEB-1999 (first entry)  
 XX DE Murine osteoclast differentiation and activation receptor.  
 XX KW Osteoprotegerin binding protein; OPG binding protein; arthritis;  
 KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;  
 KW hypercalcaemia; osteoclast differentiation and activation receptor;  
 KW Paget's disease.  
 XX OS Mus sp.  
 XX PN WO9846751-A1.  
 XX PD 22-OCT-1998.  
 XX PF 15-APR-1998; 98WO-US007594.  
 XX PR 16-APR-1997; 97US-00842842.  
 XX PR 23-JUN-1997; 97US-0080855.  
 XX PR 30-MAR-1998; 98US-00052521.  
 XX PA (AMGE-) AMGEN INC.  
 XX PI Boyle WJ;  
 XX DR WPI; 1998-594578/50.  
 XX DR N-PSDB; AAV70304.  
 XX PT Nucleic acid encoding osteoprotegerin binding protein - useful for, e.g.  
 XX PT treating bone diseases by modulating osteoclast differentiation and for  
 XX PT diagnosis.

XX PS Example 12; Fig 10; 47pp; English.  
 XX CC The present sequence represents murine osteoclast differentiation and  
 CC activation receptor (OPAR). The present invention describes  
 CC osteoprotegerin (OPG) binding protein. Host cells transfected with  
 CC vectors containing nucleic acid molecules encoding OPG binding protein  
 CC are used to produce recombinant OPG binding protein. OPG binding protein  
 CC is used in binding assays to determine osteoprotegerin (OG) in biological  
 CC samples; to screen for specific binding agents (particularly agonists and  
 CC antagonists, including intracellular proteins); to raise Ab (useful in  
 CC immunoassays for detection of OPG binding protein) and to identify  
 CC compounds that modulate binding of OPG binding protein to ODAR. The  
 CC nucleic acid molecule encoding OPG binding protein can be used to detect  
 CC OPG binding protein-encoding sequences, e.g. screening for related  
 CC sequences, also to produce transgenic animal models, while complementary

CC sequences are used for antisense regulation of OPG binding protein  
 CC expression. Modulators of OPG binding protein, particularly soluble forms  
 CC of OPG binding protein or Ab, are used to treat or prevent bone diseases,  
 CC e.g. osteoporosis, bone loss caused by arthritis or metastases,  
 CC hypercalcaemia, Paget's disease, periodontal disease, osteoporosis,  
 CC loosening of prostheses, optionally in combination with agents that  
 CC promote bone growth  
 XX SQ Sequence 625 AA;

Query Match 61.9%; Score 86; DB 2; Length 625;  
 Best Local Similarity 60.0%; Pred. No. 0.00043;  
 Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
 Db 170 CRPWTNCTLLGKLEAHQGTTSDDV 194

RESULT 37  
 AAW69958  
 ID AAW69958 standard; protein; 625 AA.  
 XX AC AAW69958;  
 XX DT 08-OCT-1998 (first entry)  
 XX DE Murine NF-kB receptor activator muRANK.  
 XX KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;  
 KW immune response; inflammatory response; toxic shock; sepsis; RANKL;  
 KW RANK ligand; tumour necrosis factor; TNF; murine.  
 XX OS Mus sp.  
 XX PN WO9828426-A2.  
 XX PD 02-JUL-1998.  
 XX PF 22-DEC-1997; 97WO-US023775.  
 XX PR 23-DEC-1996; 96US-0059978P.  
 XX PR 07-MAR-1997; 97US-00813509.  
 XX PR 14-OCT-1997; 97US-0064671P.  
 XX PA (IMMV) IMMUNEX CORP.  
 XX PI Anderson DM, Galibert LJ, Maraskovsky E;  
 XX DR WPI; 1998-377657/32.  
 XX DR N-PSDB; AAV41379.  
 XX PT New isolated ligand for receptor activator of NF-kappa B - used to  
 XX PT develop products for augmenting an immune response for inhibiting an  
 XX PT inflammatory response and for protection of cells.  
 XX PS Example 14; Page 62-64; 80pp; English.

XX CC This represents the murine muRANK (receptor activator of necrosis factor-  
 CC kappaB (NF-kB)) polypeptide which is a homolog of the human RANK. RANK is  
 CC a member of the tumour necrosis factor (TNF) family. A soluble RANK may  
 CC be used for inhibiting activation of NF-kB, by contacting a cell  
 CC expressing membrane-associated RANK with a soluble RANK which binds to  
 CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used  
 CC to induce maturation of dendritic cells and enhance their allo-  
 CC stimulatory capacity, thereby augmenting an immune response. The soluble  
 CC RANK polypeptide composition may also be used for regulating an immune or  
 CC inflammatory response. Inhibition of NF-kB by RANK antagonists may be  
 CC useful in ameliorating negative effects of an inflammatory response that  
 CC result from triggering of RANK, e.g. in treating toxic shock or sepsis,  
 CC graft-versus-host reactions, or acute inflammatory reactions. They can  
 CC also be used in adjunct therapy for disease characterised by neoplastic  
 CC cells that express RANK. RANKL polypeptides can also be used to identify



CC inhibitors of RANK and thus inhibitors of an inflammatory response, and  
CC also for protecting RANK-expressing cells from the negative effects of  
CC chemotherapy or the presence of high levels of TNF-alpha. The products  
CC can also be used for detection and drug screening  
XX  
SQ Sequence 625 AA;

Query Match 61.9%; Score 86; DB 2; Length 625;  
Best Local Similarity 60.0%; Pred. No. 0.00043;  
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTKDVV 25  
|:|||||:|:|:|||||  
Db 170 CKPWTNCTLLGKLEAHQGTTSDDV 194

RESULT 38  
AAW68294  
ID AAW68294 standard; protein; 625 AA.  
XX  
AC AAW68294;  
XX  
DT 08-OCT-1998 (first entry)  
XX  
DE Murine NF-kB receptor activator muRANK.  
XX  
KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;  
KW immune response; inflammatory response; toxic shock; sepsis; RANKL;  
KW RANK ligand; tumour necrosis factor; TNF; murine.  
XX  
OS Mus sp.  
XX  
PN WO9828424-A2.  
XX  
PD 02-JUL-1998.  
XX  
PF 22-DEC-1997; 97WO-US023866.  
XX  
PR 23-DEC-1996; 96US-0059978P.  
XX  
PR 07-MAR-1997; 97US-00813509.  
XX  
PR 14-OCT-1997; 97US-0064671P.  
XX  
PA (IMMUNEX ) IMMUNEX CORP.  
XX  
XX Anderson DM, Galibert LJ, Maraskovsky E;  
XX WPI; 1998-377655/32.  
XX N-PSDB; AAV41373.  
XX  
XX New isolated receptor activator of necrosis factor-kappa B - useful for,  
XX e.g. developing products for regulating an immune or inflammatory  
XX response, treating toxic shock or sepsis.  
XX  
XX Claim 27; Page 62-64; 80pp; English.

XX This represents the murine muRANK (receptor activator of necrosis factor-  
XX kappaB (NF-kB)) polypeptide which is a homolog of the human RANK. RANK is  
XX a member of the tumour necrosis factor (TNF) family. Host cells  
XX transformed or transfected with an expression vector comprising the RANK  
XX encoding nucleic acid can be used to produce recombinant RANK protein.  
XX The soluble RANK may be used for inhibiting activation of NF-kB, by  
XX contacting a cell expressing membrane-associated RANK with a soluble RANK  
XX which binds to RANK ligand (RANKL). The soluble RANK polypeptide  
XX composition may also be used for regulating an immune or inflammatory  
XX response. Inhibition of NF-kB by RANK antagonists may be useful in  
XX ameliorating negative effects of an inflammatory response that result  
XX from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-  
XX versus-host reactions, or acute inflammatory reactions. They can also be  
XX used in adjunct therapy for disease characterised by neoplastic cells  
XX that express RANK. The products can also be used for detection and drug  
XX screening  
XX  
XX Sequence 625 AA;

Query Match 61.9%; Score 86; DB 2; Length 625;  
Best Local Similarity 60.0%; Pred. No. 0.00043;  
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTKDVV 25  
|:|||||:|:|:|||||  
Db 170 CKPWTNCTLLGKLEAHQGTTSDDV 194

RESULT 39  
AAE08739  
ID AAE08739 standard; protein; 625 AA.  
XX  
AC AAE08739;  
XX  
DT 15-NOV-2001 (first entry)  
XX  
DE Murine receptor activator of NF kappaB (RANK) protein.  
XX  
KW Murine; receptor activator of nuclear factor kappaB; RANK; NF;  
KW tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;  
KW immune response; inflammatory response; graft-versus-host reaction;  
KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;  
KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.

OS Mus sp.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..30  
FT /label= Signal\_peptide  
FT Protein 31..625  
FT /label= Mature\_RANK\_protein  
XX  
PN US6271349-B1.  
XX  
PD 07-AUG-2001.  
XX  
PF 17-DEC-1998; 98US-00215649.  
XX  
PR 23-DEC-1996; 96US-0059978P.  
XX  
PR 23-DEC-1996; 96US-00772330.  
XX  
PR 07-MAR-1997; 97US-0077181P.  
XX  
PR 14-MAR-1997; 97US-00813509.  
XX  
PR 14-OCT-1997; 97US-0064671P.  
XX  
PR 22-DEC-1997; 97US-00996139.  
XX  
XX (IMMUNEX ) IMMUNEX CORP.  
XX  
XX Dougall WC, Galibert L;  
XX WPI; 1998-377655/32.  
XX N-PSDB; AAD15312.

XX New isolated receptor activator of necrosis factor-kappa B - useful for,  
XX e.g. developing products for regulating an immune or inflammatory  
XX response, treating toxic shock or sepsis.  
XX  
XX Example 14; Col 77-80; 47pp; English.  
XX  
XX The patent discloses novel receptor activator of nuclear factor (NF)-  
XX kappaB (RANK) proteins and their corresponding DNAs. RANK is a member of  
XX the tumour necrosis factor (TNF) receptor superfamily and associates with  
XX TNF receptor associated factor (TRAF) 2 and 3 which are important in the  
XX regulation of immune and inflammatory response. The receptors are useful  
XX for regulating immune response and in screening for inhibitors of these  
XX receptors. The cytoplasmic domain of RANK is used in developing assays  
XX for inhibitors of signal transduction, e.g. for screening the molecules  
XX that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, TRAF5 and  
XX particularly TRAF6. NF-kappaB inhibition by RANK antagonists are useful  
XX in ameliorating the negative effects of an inflammatory response that  
XX result from triggering of RANK, e.g. in treating toxic shock or sepsis,  
XX graft-versus-host reactions, acute inflammatory reactions and the effects

CC of bone resorption. RANK acts as an anti-apoptotic signal and rescue the  
 CC cells that express RANK from apoptosis. Soluble forms of the receptor are  
 CC used in vivo or in vitro based screening tests for agonists or  
 CC antagonists of RANK activity, as antagonists of RANK-mediated NF-kappa B  
 CC activation, or to inhibit transduction of a signal via RANK. RANK  
 CC compositions are used in the development of both agonistic and  
 CC antagonistic antibodies, or as an adjunct therapy for disease  
 CC characterised by neoplastic cells that express RANK. Compounds that  
 CC interfere with RANK/TRAF6 interactions are useful for modulating the  
 CC formation of osteoclasts from osteoclast precursors and for modulating the  
 CC osteoclast function and activities. They are used as inhibitors of  
 CC diseases associated with excess bone resorption and as immunosuppressants  
 CC or anti-inflammatory agents. The RANK DNAs are useful for the expression  
 CC of recombinant proteins, as probes for analysis of the presence or  
 CC distribution of RANK transcripts, while the proteins are useful in  
 CC preparing kits for the detection of soluble RANK, or monitor RANK-related  
 CC activity. The present sequence is RANK protein from murine  
 XX  
 SQ Sequence 625 AA;

Query Match 61.9%; Score 86; DB 2; Length 625;  
 Best Local Similarity 60.0%; Pred. No. 0.00043;  
 Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
 Db 170 CRPWTNCTLLGKLEAHQGTESDVV 194

RESULT 40  
 AAY53649  
 ID AAY53649 standard; protein; 625 AA.  
 AC AAY53649;  
 XX  
 DT 22-FEB-2000 (first entry)  
 XX  
 DE A mouse receptor activator of NF-kappaB designated RANK.  
 XX  
 KW Mouse; receptor; RANK; Receptor activator of NF-kappaB;  
 KW osteoclast activity; immune response; inflammatory response;  
 KW excess bone resorption; osteoclast generation; bone loss; osteoporosis;  
 KW Paget's disease; bone cancer; cancer; hypercalcemia; osteoclastogenesis;  
 KW metastasising cancer; osteoclast differentiation; signal transduction.  
 OS Mus sp.  
 XX  
 FN WO9958674-A2.  
 XX  
 PD 18-NOV-1999.  
 XX  
 PF 13-MAY-1999; 99WO-US010588.  
 XX  
 PR 14-MAY-1998; 98US-0085487P.  
 PR 03-DEC-1998; 98US-0110836P.  
 XX  
 PA (IMMV) IMMUNEX CORP.  
 XX  
 PI Anderson DM, Galibert LJ;  
 XX  
 DR WPI: 2000-053099/04.  
 DR N-PSDB; AAZ36258.  
 XX  
 PT Novel cytokine receptors for regulating osteoclast activity to ameliorate  
 PT excess bone loss effects of osteoporosis, Paget's disease, bone cancers  
 PT etc.  
 XX  
 PS Disclosure; Page 25-27; 28pp; English.  
 XX  
 CC The present sequence represents a soluble murine receptor designated RANK  
 CC (Receptor activator of NF-kappaB). The protein is used to regulate  
 CC osteoclast activity. The RANK protein or its fragments are useful for  
 CC regulating an immune or inflammatory response, especially to decrease

CC excess bone resorption, and for inhibiting osteoclast activity,  
 CC regulating osteoclast generation and inhibiting osteoclast generation in  
 CC individuals inflicted with excess bone resorption. Especially, the RANK  
 CC protein is used to treat individuals at risk for excess bone loss,  
 CC osteoporosis, Paget's disease, bone cancer and cancers associated with  
 CC hypercalcemia. The RANK protein ameliorates the effects of excess bone  
 CC loss, by binding to its ligand and inhibiting binding of other cells  
 CC expressing RANK. It thus decreases osteoclastogenesis when administered  
 CC into metastasising cancers such as breast cancer, multiple myeloma,  
 CC melanomas, lung cancer, prostate, hematologic, head and neck, and renal  
 CC which metastasise to bone and induce bone breakdown by locally disrupting  
 CC normal bone remodelling, by disrupting the osteoclast differentiation  
 CC pathway. This results in the reduction in the number of osteoclasts,  
 CC lesser bone resorption and relief from the negative effects of  
 CC hypercalcemia. The RANK protein also ameliorates systemic effects by  
 CC interfering with I/II signal transduction that leads to the  
 CC differentiation of osteoclast precursors into osteoclasts  
 XX  
 SQ Sequence 625 AA;

Query Match 61.9%; Score 86; DB 3; Length 625;  
 Best Local Similarity 60.0%; Pred. No. 0.00043;  
 Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
 Db 170 CRPWTNCTLLGKLEAHQGTESDVV 194

Search completed: May 5, 2004, 14:38:05  
 Job time : 13.4144 secs

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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:35:32 ; Search time 3.59589 Seconds  
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358.923 Million cell updates/sec

Title: US-10-067-122B-2\_COPY\_133\_157  
Perfect score: 139  
Sequence: 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/iaa/5A COMB.pep.\*  
2: /cgn2\_6/prodata/2/iaa/5B COMB.pep.\*  
3: /cgn2\_6/prodata/2/iaa/6A COMB.pep.\*  
4: /cgn2\_6/prodata/2/iaa/6B COMB.pep.\*  
5: /cgn2\_6/prodata/2/iaa/6C COMB.pep.\*  
6: /cgn2\_6/prodata/2/iaa/6D COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	139	100.0	191	3	US-08-974-022-52
2	139	100.0	191	3	US-08-795-445A-52
3	139	100.0	191	3	US-08-795-447A-52
4	139	100.0	191	3	US-08-974-186-52
5	139	100.0	191	3	US-08-795-446B-52
6	139	100.0	191	4	US-08-706-945D-139
7	139	100.0	191	4	US-08-577-788C-53
8	139	100.0	256	1	US-08-236-918A-6
9	139	100.0	256	4	US-08-150-864A-6
10	139	100.0	256	4	US-08-012-269A-2
11	139	100.0	256	4	US-09-623-545A-3
12	139	100.0	256	5	PCT-US96-03965-2
13	115	82.7	132	4	US-09-523-323-55
14	115	82.7	219	2	US-08-816-605-2
15	115	82.7	255	1	US-08-236-918A-8
16	115	82.7	255	2	US-08-816-605-9
17	115	82.7	255	3	US-09-006-353A-11
18	115	82.7	255	4	US-09-007-097-2
19	115	82.7	255	4	US-09-150-864A-8
20	115	82.7	255	4	US-09-573-986-11
21	115	82.7	255	4	US-09-578-764A-2
22	115	82.7	255	4	US-09-623-545A-2
23	115	82.7	255	5	PCT-US96-03965-8
24	86	61.9	625	3	US-08-996-139-15
25	86	61.9	625	3	US-08-995-659-15
26	86	61.9	625	3	US-09-215-649A-15
27	86	61.9	625	4	US-09-577-780-15

28	86	61.9	625	4	US-09-577-800-15	Sequence 15, Appl
29	86	61.9	625	4	US-09-466-496-15	Sequence 15, Appl
30	86	61.9	625	4	US-09-871-856-15	Sequence 15, Appl
31	86	61.9	625	4	US-09-871-291-15	Sequence 15, Appl
32	86	61.9	625	4	US-09-877-650-15	Sequence 15, Appl
33	75	54.0	451	3	US-08-996-139-4	Sequence 4, Appl
34	75	54.0	451	3	US-08-995-659-4	Sequence 4, Appl
35	75	54.0	451	3	US-09-215-649A-4	Sequence 4, Appl
36	75	54.0	451	4	US-09-577-780-4	Sequence 4, Appl
37	75	54.0	451	4	US-09-466-496-4	Sequence 4, Appl
38	75	54.0	451	4	US-09-871-856-4	Sequence 4, Appl
39	75	54.0	451	4	US-09-871-291-4	Sequence 4, Appl
40	75	54.0	451	4	US-09-877-650-4	Sequence 4, Appl
41	75	54.0	451	4	US-09-877-650-4	Sequence 4, Appl
42	75	54.0	591	3	US-08-996-139-2	Sequence 2, Appl
43	75	54.0	591	3	US-08-995-659-2	Sequence 2, Appl
44	75	54.0	591	3	US-09-215-649A-2	Sequence 2, Appl
45	75	54.0	591	4	US-09-577-780-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-974-022-52  
; Sequence 52, Application US/08974022  
; Patent No. 6015938  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Behavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,022  
; FILING DATE: 12-DEC-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/577,788  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 191 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-974-022-52

Query Match 100.0%; Score 139; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 5.6e-14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25

DB 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

## RESULT 2

US-08-795-445A-52  
; Sequence 52, Application US/08795445A  
; Patent No. 6284485  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/795,445A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/577,788  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 191 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-795-445A-52

Query Match 100.0%; Score 139; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 5.6e-14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
DB 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

## RESULT 3

US-08-795-447A-52  
; Sequence 52, Application US/08795447A  
; Patent No. 6284728  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: Osteoprotegerin  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: One Amgen Center Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91362-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

Query Match 100.0%; Score 139; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 5.6e-14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,447A  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378D2  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 191 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-795-447A-52

Query Match 100.0%; Score 139; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 5.6e-14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
DB 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

## RESULT 4

US-08-974-186-52  
; Sequence 52, Application US/08974186  
; Patent No. 6284740  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,186  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/577,788  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 191 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-974-186-52

Query Match 100.0%; Score 139; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 5.6e-14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 139; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 5.6e-14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

## RESULT 5

US-08-795-446B-52  
; Sequence 52, Application US/08795446B  
; Patent No. 6285032  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 DeHavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/795,446B  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/577,788  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 191 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-795-446B-52

Query Match 100.0%; Score 139; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 5.6e-14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

## RESULT 6

US-08-706-945D-139  
; Sequence 139, Application US/08706945D  
; Patent No. 6369027  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William  
; APPLICANT: Lacey, David  
; APPLICANT: Calzone, Frank  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: Osteoprotegerin  
; FILE REFERENCE: A-378CIP  
; CURRENT APPLICATION NUMBER: US/08/706,945D  
; CURRENT FILING DATE: 1996-09-03  
; PRIOR APPLICATION NUMBER: 08/577,788  
; PRIOR FILING DATE: 1995-12-22  
; NUMBER OF SEQ ID NOS: 145  
; SOFTWARE: Patent in version 3.1

; SEQ ID NO 139  
; LENGTH: 191  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-706-945D-139

Query Match 100.0%; Score 139; DB 4; Length 191;  
Best Local Similarity 100.0%; Pred. No. 5.6e-14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

## RESULT 7

US-08-577-788C-53  
; Sequence 53, Application US/08577788C  
; Patent No. 6613544  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William  
; APPLICANT: Lacey, David  
; APPLICANT: Calzone, Frank  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: Osteoprotegerin  
; FILE REFERENCE: A-378 Rev.  
; CURRENT APPLICATION NUMBER: US/08/577,788C  
; CURRENT FILING DATE: 1995-12-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: Patent In version 3.1  
; SEQ ID NO 53  
; LENGTH: 191  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-08-577-788C-53

Query Match 100.0%; Score 139; DB 4; Length 191;  
Best Local Similarity 100.0%; Pred. No. 5.6e-14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

## RESULT 8

US-08-236-918A-6  
; Sequence 6, Application US/08236918A  
; Patent No. 5674704  
; GENERAL INFORMATION:  
; APPLICANT: Alderson, Mark R.  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple 7.5.3  
; SOFTWARE: Microsoft Word, Version #6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/236,918A  
; FILING DATE: 06-May-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/060,843

```
/ FILING DATE: 07-May-1993
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Anderson, Kathryn A.
/ REGISTRATION NUMBER: 32,172
/ REFERENCE/DOCKET NUMBER: 2801-B
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 587-0430
/ TELEFAX: (206) 233-0644
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 256 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-236-918A-6

Query Match      100.0%; Score 139; DB 1; Length 256;
Best Local Similarity 100.0%; Pred. No. 7.9e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 9
US-09-150-864A-6
; Sequence 6, Application US/09150864A
; Patent No. 6355779
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand and Human Receptor
; TITLE OF INVENTION: That Binds Thereto
; FILE REFERENCE: 2801-B
; CURRENT APPLICATION NUMBER: US/09/150,864A
; CURRENT FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 08/060,843
; PRIOR FILING DATE: 1993-05-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus sp. (clone: mu4-1BB)
US-09-150-864A-6

Query Match      100.0%; Score 139; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 7.9e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 10
US-08-012-269A-2
; Sequence 2, Application US/08012269A
; Patent No. 6362325
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung S.
; TITLE OF INVENTION: MURINE
; FILE REFERENCE: 740,009US1
; CURRENT APPLICATION NUMBER: US/08/012,269A
; CURRENT FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: US 07/922,996
; PRIOR FILING DATE: 1992-07-30
; PRIOR APPLICATION NUMBER: US 07/267,572
; PRIOR FILING DATE: 1988-11-07
; NUMBER OF SEQ ID NOS: 13

Query Match      100.0%; Score 139; DB 1; Length 256;
Best Local Similarity 100.0%; Pred. No. 7.9e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 11
US-09-623-545A-3
; Sequence 3, Application US/09623545A
; Patent No. 6627200
; GENERAL INFORMATION:
; APPLICANT: Merckle GmbH
; TITLE OF INVENTION: UTILIZATION OF CD137 IN ORDER TO PROMOTE THE
; TITLE OF INVENTION: PROLIFERATION OF PERIPHERAL MONOCYTES
; FILE REFERENCE: 30424.IUSWO
; CURRENT APPLICATION NUMBER: US/09/623,545A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: EPO 98103859.9
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/EP99/01440
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-623-545A-3

Query Match      100.0%; Score 139; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 7.9e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 12
PCT-US96-03965-2
; Sequence 2, Application PC/TUS9603965
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung Se
; APPLICANT: Kang, Chang-Yuill
; TITLE OF INVENTION: Monoclonal antibody against human
; TITLE OF INVENTION: receptor 4-1BB
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnard, Brown & Michaels
; STREET: 306 East State Street, Suite 220
; CITY: Ithaca
; STATE: NY
; COUNTRY: USA
; ZIP: 14850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/03965
; FILING DATE:
; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,796
; FILING DATE: 16-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012,269
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/922,996
; FILING DATE: 30-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/267,577
; FILING DATE: 07-NOV-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Michaels, Christopher A
; REGISTRATION NUMBER: 34,390
; REFERENCE/DOCKET NUMBER: KW05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 607-273-1711
; TELEFAX: 607-273-2609
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-03965-2

Query Match      100.0%; Score 139; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 7.9e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
DB      133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

RESULT 13
US-09-523-323-55
; Sequence 55, Application US/09523323
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; APPLICANT: Ullrich, Stephen
; APPLICANT: Zhai, Yifan
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1488.065000C
; CURRENT APPLICATION NUMBER: US/09/523,323
; CURRENT FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: 60/168,380
; EARLIER FILING DATE: 1999-12-02
; EARLIER APPLICATION NUMBER: 60/148,326
; EARLIER FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: 60/142,657
; EARLIER FILING DATE: 1999-07-06
; EARLIER APPLICATION NUMBER: 60/137,457
; EARLIER FILING DATE: 1999-06-04
; EARLIER APPLICATION NUMBER: 60/124,041
; EARLIER FILING DATE: 1998-03-11
; EARLIER APPLICATION NUMBER: 09/252,656
; EARLIER FILING DATE: 1999-02-19
; EARLIER APPLICATION NUMBER: 60/075,409
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 09/027,287
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 09/003,886
; EARLIER FILING DATE: 1998-01-07
; EARLIER APPLICATION NUMBER: 08/822,953
; EARLIER FILING DATE: 1997-03-21
; EARLIER APPLICATION NUMBER: 60/013,923
; EARLIER FILING DATE: 1996-03-22
; EARLIER APPLICATION NUMBER: 60/030,157

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; EARLIER FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 55
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-523-323-55

Query Match      82.7%; Score 115; DB 4; Length 132;
Best Local Similarity 80.0%; Pred. No. 2e-10;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
DB      106 CRPWTNCSLDGRSVLVTGKTKRDVV 130

RESULT 14
US-08-816-605-2
; Sequence 2, Application US/08816605
; Patent No. 5874240
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human 4-TBB Receptor Splicing Variant
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,605
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PR254
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-816-605-2

Query Match      82.7%; Score 115; DB 2; Length 219;
Best Local Similarity 80.0%; Pred. No. 3.7e-10;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
DB      97 CRPWTNCSLDGRSVLVTGKTKRDVV 121

RESULT 15
US-08-236-918A-8
; Sequence 8, Application US/08236918A
; Patent No. 5674704
; GENERAL INFORMATION:

```

APPLICANT: Alderson, Mark R.  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple 7.5.3  
SOFTWARE: Microsoft Word, Version #6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/236,918A  
FILING DATE: 06-May-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/060,843  
FILING DATE: 07-May-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2801-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-236-918A-8

Query Match 82.7%; Score 115; DB 1; Length 255;  
Best Local Similarity 80.0%; Pred. No. 4.4e-10;  
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTKDVV 25  
DB 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 16  
US-08-816-605-9  
Sequence 9, Application US/08816605  
Patent No. 5874240  
GENERAL INFORMATION:  
APPLICANT: Ni, Jian  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Gentz, Reiner  
TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/816,605

FILING DATE: 13-MAR-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF254  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8512  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-816-605-9

Query Match 82.7%; Score 115; DB 2; Length 255;  
Best Local Similarity 80.0%; Pred. No. 4.4e-10;  
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTKDVV 25  
DB 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 17  
US-09-006-353A-11  
Sequence 11, Application US/09006353A  
Patent No. 6261801  
GENERAL INFORMATION:  
APPLICANT: WEI, YING-FEI  
APPLICANT: YU, GUO-LIANG  
APPLICANT: GENTZ, REINER  
APPLICANT: RUBEN, STEVEN  
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/006,353A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOKES, ANDERS A  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF341  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-006-353A-11

Query Match 82.7%; Score 115; DB 3; Length 255;  
Best Local Similarity 80.0%; Pred. No. 4.4e-10;  
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;



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; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/09/573,986
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-573-986-11

Query Match      82.7%; Score 115; DB 4; Length 255;
Best Local Similarity 80.0%; Pred. No. 4.4e-10;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
DB 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 21
US-09-578-764A-2
; Sequence 2, Application US/09578764A
; Patent No. 6569997
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung
; TITLE OF INVENTION: METHOD OF USING HUMAN RECEPTOR PROTEIN 4-1BB
; FILE REFERENCE: 740.011US1
; CURRENT APPLICATION NUMBER: US/09/578,764A
; CURRENT FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-578-764A-2

Query Match      82.7%; Score 115; DB 4; Length 255;
Best Local Similarity 80.0%; Pred. No. 4.4e-10;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
DB 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 22
US-09-623-545A-2
; Sequence 2, Application US/09623545A
; Patent No. 6627200
; GENERAL INFORMATION:
; APPLICANT: Merckle GmbH
; TITLE OF INVENTION: UTILIZATION OF CD137 IN ORDER TO PROMOTE THE
; FILE REFERENCE: 30424.1USNO
; CURRENT APPLICATION NUMBER: US/09/623,545A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: EPO 98103859.9
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/EP99/01440
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-623-545A-2

Query Match      82.7%; Score 115; DB 4; Length 255;
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; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,659
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA: USN 60/064,671
; APPLICATION NUMBER: USN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/813,509
; FILING DATE: 07 MARCH 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-995-659-15

Query Match 61.9%; Score 86; DB 3; Length 625;
Best Local Similarity 60.0%; Pred. No. 4.2e-05;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPTNCSLDGRSVLKTGTTEKDVV 25
Db 170 CKPWTNCTLLGKLEAHQGTESDVG 194

RESULT 26
US-09-215-649A-15
; Sequence 15, Application US/09215649A
; Patent No. 6271349
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,649A
; FILING DATE: 17-Dec-1998
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <unknown>

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; APPLICATION NUMBER: USN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-215-649A-15

Query Match 61.9%; Score 86; DB 3; Length 625;
Best Local Similarity 60.0%; Pred. No. 4.2e-05;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPTNCSLDGRSVLKTGTTEKDVV 25
Db 170 CKPWTNCTLLGKLEAHQGTESDVG 194

RESULT 27
US-09-577-780-15
; Sequence 15, Application US/09577780
; Patent No. 6419929
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/577,780
; FILING DATE: 24-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid

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;;  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation, Law Department  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/871.856  
; FILING DATE: 31-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/996,139  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: USN 08/813,509  
; FILING DATE: 07 MARCH 1997  
; APPLICATION NUMBER: USN 08/772,330  
; FILING DATE: 23 DECEMBER 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia Anne  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2851-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 625 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-871-856-15  
  
Query Match 61.9%; Score 86; DB 4; Length 625;  
Best Local Similarity 60.0%; Pred.No. 4.2e-05;  
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
  
QY 1 CRPWNCSLDGRSVLKTGTTEKDVV 25  
Db 170 CKPWNCTLLGKLEAHQGTTESDVV 194  
  
RESULT 31  
US-09-871-291-15  
; Sequence 15, Application US/09871291  
; Patent No. 6562948  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Dirk M.  
; Galibert, Laurent  
; Maraskovsky, Eugene  
; TITLE OF INVENTION: Receptor Activator of NF-kappaB  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation, Law Department  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/871.291  
; FILING DATE: 30-May-2001

;;  
; CLASSIFICATION: <Unknown>  
; APPLICATION NUMBER: 08/996,139  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: USN 08/813,509  
; FILING DATE: 07 MARCH 1997  
; APPLICATION NUMBER: USN 08/772,330  
; FILING DATE: 23 DECEMBER 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia Anne  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2851-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 625 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-871-291-15  
  
Query Match 61.9%; Score 86; DB 4; Length 625;  
Best Local Similarity 60.0%; Pred.No. 4.2e-05;  
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
  
QY 1 CRPWNCSLDGRSVLKTGTTEKDVV 25  
Db 170 CKPWNCTLLGKLEAHQGTTESDVV 194  
  
RESULT 32  
US-09-877-650-15  
; Sequence 15, Application US/09877650  
; Patent No. 6649164  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Dirk M.  
; Galibert, Laurent  
; Maraskovsky, Eugene  
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation, Law Department  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/877,650  
; FILING DATE: 08-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/995,659  
; FILING DATE: 1997-12-22  
; APPLICATION NUMBER: USN 08/813,509  
; FILING DATE: 07 MARCH 1997  
; APPLICATION NUMBER: USN 08/772,330  
; FILING DATE: 23 DECEMBER 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia Anne  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2852-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 625 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-877-650-15

Query Match 61.9%; Score 86; DB 4; Length 625;  
Best Local Similarity 60.0%; Pred. No. 4.2e-05;  
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
DB 170 CKPWTNCTLLGKLEAHQGTTSDDV 194

RESULT 33  
US-08-996-139-4  
; Sequence 4, Application US/08996139  
; Patent No. 6017729  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Dirk M.  
; APPLICANT: Galibert, Laurent  
; APPLICANT: Maraskovsky, Eugene  
; TITLE OF INVENTION: Receptor Activator of NF-kappaB  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation, Law Department  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/996,139  
; FILING DATE: 22 DECEMBER 1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 60/064,671  
; FILING DATE: 14 OCTOBER 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/813,509  
; FILING DATE: 07 MARCH 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/772,330  
; FILING DATE: 23 DECEMBER 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia Anne  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2851-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 451 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-996-139-4

Query Match 54.0%; Score 75; DB 3; Length 451;  
Best Local Similarity 52.0%; Pred. No. 0.0015;  
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25

DB 169 CRPWTNCTFLGRVBEHGHGTEKSDAV 193

RESULT 34  
US-08-995-659-4  
; Sequence 4, Application US/08995659  
; Patent No. 6242213  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Dirk M.  
; APPLICANT: Galibert, Laurent  
; APPLICANT: Maraskovsky, Eugene  
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation, Law Department  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/995,659  
; FILING DATE: 22 DECEMBER 1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 60/064,671  
; FILING DATE: 14 OCTOBER 1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/813,509  
; FILING DATE: 07 MARCH 1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/772,330  
; FILING DATE: 23 DECEMBER 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia Anne  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2852-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 451 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-995-659-4

Query Match 54.0%; Score 75; DB 3; Length 451;  
Best Local Similarity 52.0%; Pred. No. 0.0015;  
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
DB 169 CRPWTNCTFLGRVBEHGHGTEKSDAV 193

RESULT 35  
US-09-215-649A-4  
; Sequence 4, Application US/09215649A  
; Patent No. 6271349  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Dirk M.  
; APPLICANT: Galibert, Laurent

Maraskovsky, Eugene  
TITLE OF INVENTION: Receptor Activator of NF-kappaB  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation, Law Department  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/215,649A  
FILING DATE: 17-Dec-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/996,139  
FILING DATE: <Unknown>  
APPLICATION NUMBER: USN 08/813,509  
FILING DATE: 07 MARCH 1997  
APPLICATION NUMBER: USN 08/772,330  
FILING DATE: 23 DECEMBER 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2851-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 451 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-215-649A-4  
Query Match 54.0%; Score 75; DB 3; Length 451;  
Best Local Similarity 52.0%; Pred. No. 0.0015; 9; Indels 0; Gaps 0;  
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;  
QY 1 CRPTNCSLDGRSVLKTGTTEKDV 25  
|||||:|:|:|:|  
Db 169 CRPTNCTFLGKRVHGHGTEKSDAV 193  
RESULT 36  
US-09-577-780-4  
Sequence 4, Application US/09577780  
Patent No. 6419929  
GENERAL INFORMATION:  
APPLICANT: Anderson, Dirk M.  
Galibert, Laurent  
Maraskovsky, Eugene  
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation, Law Department  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/577,780  
FILING DATE: 24-May-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/995,659  
FILING DATE: <Unknown>  
APPLICATION NUMBER: USN 08/813,509  
FILING DATE: 07 MARCH 1997  
APPLICATION NUMBER: USN 08/772,330  
FILING DATE: 23 DECEMBER 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2852-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 451 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-577-780-4  
Query Match 54.0%; Score 75; DB 4; Length 451;  
Best Local Similarity 52.0%; Pred. No. 0.0015; 9; Indels 0; Gaps 0;  
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;  
QY 1 CRPTNCSLDGRSVLKTGTTEKDV 25  
|||||:|:|:|:|  
Db 169 CRPTNCTFLGKRVHGHGTEKSDAV 193  
RESULT 37  
US-09-577-800-4  
Sequence 4, Application US/09577800  
Patent No. 6479635  
GENERAL INFORMATION:  
APPLICANT: Anderson, Dirk M.  
Galibert, Laurent  
Maraskovsky, Eugene  
TITLE OF INVENTION: Receptor Activator of NF-kappaB  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation, Law Department  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/577,800  
FILING DATE: 24-MAY-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/996,139  
FILING DATE: 22 DECEMBER 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USN 60/064,671  
FILING DATE: 14 OCTOBER 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USN 08/813,509  
FILING DATE: 07 MARCH 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USN 08/772,330

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/ FILING DATE: 23 DECEMBER 1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Perkins, Patricia Anne
/ REGISTRATION NUMBER: 34,693
/ REFERENCE/DOCKET NUMBER: 2851-A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206)587-0430
/ TELEFAX: (206)233-0644
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 451 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-577-800-4

Query Match          54.0%; Score 75; DB 4; Length 451;
Best Local Similarity 52.0%; Pred. No. 0.0015;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 169 CRPWTNCTFLGKRVHHGTEKSDAV 193

RESULT 38
US-09-466-496-4
; Sequence 4, Application US/09466496
; Patent No. 6528482
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/466,496
; FILING DATE: 17-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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/ SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-466-496-4

Query Match          54.0%; Score 75; DB 4; Length 451;
Best Local Similarity 52.0%; Pred. No. 0.0015;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 169 CRPWTNCTFLGKRVHHGTEKSDAV 193

RESULT 39
US-09-871-856-4
; Sequence 4, Application US/09871856
; Patent No. 6537763
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,856
; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-871-856-4

Query Match          54.0%; Score 75; DB 4; Length 451;
Best Local Similarity 52.0%; Pred. No. 0.0015;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 169 CRPWTNCTFLGKRVHHGTEKSDAV 193

RESULT 40
US-09-871-291-4
; Sequence 4, Application US/09871291
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; Patent No. 6552948
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,291
; FILING DATE: 30-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-871-291-4

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Query Match 54.0%; Score 75; DB 4; Length 451;  
Best Local Similarity 52.0%; Pred. No. 0.0015;  
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CRPWTNCSLDGRSVLKTGTEKDVV 25  
|||||: | | | | |  
Db 169 CRPWTNCTFLGKRVEHHGTEKSDAV 193

Search completed: May 5, 2004, 14:42:17  
Job time : 4.59589 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:40:42 ; Search time 9.24658 Seconds  
(without alignments)  
749.438 Million cell updates/sec

Title: US-10-067-122B-2\_COPY\_133\_157  
Perfect score: 139  
Sequence: 1 CRPWTNCLDGRSVLKTGTEDVV 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

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- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
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- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
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- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	191	11	US-09-405-032-136
2	139	100.0	256	13	Sequence 136, App
3	139	100.0	256	14	Sequence 10, Appl
4	115	82.7	132	15	US-10-067-122-2
5	115	82.7	219	9	Sequence 55, Appl
6	115	82.7	219	13	Sequence 2, Appl
7	115	82.7	255	9	Sequence 2, Appl
8	115	82.7	255	9	Sequence 9, Appl
9	115	82.7	255	9	Sequence 11, Appl
10	115	82.7	255	10	Sequence 13, Appl
11	115	82.7	255	13	US-09-877-336-2
12	115	82.7	255	13	Sequence 2, Appl
13	115	82.7	255	14	Sequence 2, Appl
14	115	82.7	255	14	Sequence 11, Appl
15	115	82.7	255	14	Sequence 160, App

16	115	82.7	255	15	US-10-418-242-13
17	86	61.9	625	9	US-09-871-856-15
18	86	61.9	625	9	US-09-877-650-15
19	86	61.9	625	12	US-09-865-363-15
20	86	61.9	625	12	US-10-151-071-2
21	86	61.9	625	12	US-09-957-944-4
22	86	61.9	625	14	US-10-166-232A-2
23	86	61.9	625	14	US-10-405-878-15
24	79	56.8	615	9	US-09-768-779A-2
25	79	56.8	615	14	US-10-291-480-2
26	75	54.0	443	12	US-10-151-071-5
27	75	54.0	443	14	US-10-166-232A-5
28	75	54.0	451	9	US-09-871-856-4
29	75	54.0	451	9	US-09-877-650-4
30	75	54.0	451	12	US-09-865-363-4
31	75	54.0	451	14	US-10-405-878-4
32	75	54.0	591	9	US-09-871-856-2
33	75	54.0	591	9	US-09-877-650-2
34	75	54.0	591	12	US-09-865-363-2
35	75	54.0	591	14	US-10-405-878-2
36	75	54.0	616	9	US-09-871-856-6
37	75	54.0	616	9	US-09-877-650-6
38	75	54.0	616	12	US-09-865-363-6
39	75	54.0	616	12	US-10-151-071-4
40	75	54.0	616	12	US-09-957-944-2
41	75	54.0	616	14	US-10-166-232A-4
42	75	54.0	622	12	US-10-405-878-6
43	75	54.0	622	12	US-09-957-944-10
44	73	52.5	138	13	US-10-112-793-20
45	73	52.5	274	9	US-09-836-607-3

ALIGNMENTS

RESULT 1

US-09-405-032-136  
; Sequence 136, Application US/09405032  
; Publication No. US2003020782/A1  
; GENERAL INFORMATION:  
; APPLICANT: Amgen Inc.  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 168  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Behavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: United States  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/405,032  
; FILING DATE: 24-Sep-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378-CIP2  
; INFORMATION FOR SEQ ID NO: 136:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 191 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 136:  
US-09-405-032-136  
Query Match 100.0%; Score 139; DB 11; Length 191;

Best Local Similarity 100.0%; Pred. No. 6.9e-13;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

## RESULT 2

US-10-027-199-10  
; Sequence 10, Application US/10027199  
; Publication No. US20020168719A1  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung  
; TITLE OF INVENTION: NEW RECEPTOR AND RELATED PRODUCTS AND  
; FILE REFERENCE: 740.013US2  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR FILING DATE: 1997-10-22  
; PRIOR APPLICATION NUMBER: 08/955,572  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-22  
; PRIOR APPLICATION NUMBER: 08/461,652  
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-06-05  
; PRIOR APPLICATION NUMBER: 08/122,796  
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-09-03  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-027-199-10

Query Match 100.0%; Score 139; DB 13; Length 256;  
Best Local Similarity 100.0%; Pred. No. 9.5e-13;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

## RESULT 3

US-10-067-122-2  
; Sequence 2, Application US/10067122  
; Publication No. US20030100745A1  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung S.  
; TITLE OF INVENTION: MURINE 4-1BB GENE  
; FILE REFERENCE: 740.009US1  
; CURRENT FILING DATE: 2002-02-04  
; PRIOR FILING DATE: 1993-02-01  
; PRIOR APPLICATION NUMBER: 08/012,269  
; PRIOR FILING DATE: 1992-07-30  
; PRIOR APPLICATION NUMBER: US 07/922,996  
; PRIOR FILING DATE: 1998-11-07  
; PRIOR APPLICATION NUMBER: US 07/267,572  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-067-122-2

Query Match 100.0%; Score 139; DB 14; Length 256;  
Best Local Similarity 100.0%; Pred. No. 9.5e-13;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

## RESULT 4

US-10-375-680-55  
; Sequence 55, Application US/10375680  
; Publication No. US20040009147A1  
; GENERAL INFORMATION:  
; APPLICANT: Ebner, Reinhard  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ruben, Steven M  
; APPLICANT: Ullrich, Stephen  
; APPLICANT: Zhai, Yifan  
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use  
; FILE REFERENCE: 1488.065000B  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 60/360,234  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 55  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-375-680-55

Query Match 82.7%; Score 115; DB 15; Length 132;  
Best Local Similarity 80.0%; Pred. No. 2e-09;  
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
Db 106 CRPWTNCSLDGRSVLKTGTTEKDVV 130

## RESULT 5

US-09-739-394-2  
; Sequence 2, Application US/09739394  
; Patent No. US20010014465A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; YU, Guo-Liang  
; Gentz, Reiner  
; TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/739,394  
; FILING DATE: 19-Dec-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/253,549  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF254  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8512  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 219 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-739-394-2

Query Match      82.7%; Score 115; DB 9; Length 219;
Best Local Similarity 80.0%; Pred. No. 3.4e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTKRDVV 25
Db 97 CRPWTNCSLDGKSVLVNGTKERDVV 121

RESULT 6
US-10-097-330-2
; Sequence 2, Application US/10097330
; Publication No. US20020127651A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: HUMAN 4-1BB RECEPTOR SPLICING VARIANT
; FILE REFERENCE: PF254D1C2
; CURRENT APPLICATION NUMBER: US/10/097.330
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 09/739,394
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/253,549
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: US 08/816,605
; PRIOR FILING DATE: 1997-03-13
; PRIOR APPLICATION NUMBER: US 60/013,474
; PRIOR FILING DATE: 1996-03-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-330-2

Query Match      82.7%; Score 115; DB 13; Length 219;
Best Local Similarity 80.0%; Pred. No. 3.4e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTKRDVV 25
Db 97 CRPWTNCSLDGKSVLVNGTKERDVV 121

RESULT 7
US-09-739-394-9
; Sequence 9, Application US/09739394
; Patent No. US20010014465A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; Yu, Guo-Liang
; Gentz, Reiner
; TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/739,394
; FILING DATE: 19-Dec-2000
; CLASSIFICATION: <UNKNOWN>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/253,549
; FILING DATE: <UNKNOWN>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF254
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-739-394-9

Query Match      82.7%; Score 115; DB 9; Length 255;
Best Local Similarity 80.0%; Pred. No. 4e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTKRDVV 25
Db 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 8
US-09-826-212-11
; Sequence 11, Application US/09826212
; Patent No. US20010021516A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Pei
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; APPLICANT: Ni, Jian
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280006
; CURRENT APPLICATION NUMBER: US/09/826,212
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 11
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-212-11

Query Match      82.7%; Score 115; DB 9; Length 255;
Best Local Similarity 80.0%; Pred. No. 4e-09;
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTKRDVV 25
Db 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 9
US-09-935-727-13
; Sequence 13, Application US/09935727
; Patent No. US20020150593A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P2
; CURRENT APPLICATION NUMBER: US/09/935,727
; CURRENT FILING DATE: 2001-08-24

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; PRIOR APPLICATION NUMBER: 60/303,224  
 ; PRIOR FILING DATE: 2001-07-06  
 ; PRIOR APPLICATION NUMBER: 60/252,131  
 ; PRIOR FILING DATE: 2000-11-21  
 ; PRIOR APPLICATION NUMBER: 60/227,598  
 ; PRIOR FILING DATE: 2000-08-25  
 ; PRIOR APPLICATION NUMBER: 09/518,931  
 ; PRIOR FILING DATE: 2000-03-03  
 ; PRIOR APPLICATION NUMBER: 60/168,235  
 ; PRIOR FILING DATE: 1999-12-01  
 ; PRIOR APPLICATION NUMBER: 60/146,371  
 ; PRIOR FILING DATE: 1999-08-02  
 ; PRIOR APPLICATION NUMBER: 60/131,964  
 ; PRIOR FILING DATE: 1999-04-30  
 ; PRIOR APPLICATION NUMBER: 60/131,270  
 ; PRIOR FILING DATE: 1999-04-27  
 ; PRIOR APPLICATION NUMBER: 60/124,092  
 ; PRIOR FILING DATE: 1999-03-12  
 ; PRIOR APPLICATION NUMBER: 60/121,774  
 ; PRIOR FILING DATE: 1999-03-04  
 ; PRIOR APPLICATION NUMBER: 09/006,352  
 ; PRIOR FILING DATE: 1998-01-13  
 ; PRIOR APPLICATION NUMBER: 60/035,496  
 ; PRIOR FILING DATE: 1997-01-14  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 13  
 ; LENGTH: 255  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-935-727-13

Query Match 82.7%; Score 115; DB 9; Length 255;  
 Best Local Similarity 80.0%; Pred. No. 4e-09;  
 Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
 DB 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 10  
 US-09-877-336-2  
 ; Sequence 2, Application US/09877336  
 ; Publication No. US2003000851A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kwon, Byoung  
 ; TITLE OF INVENTION: METHODS OF USING HUMAN RECEPTOR ON  
 ; FILE REFERENCE: 740.011U3  
 ; CURRENT APPLICATION NUMBER: US/09/877,336  
 ; PRIOR FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: 09/007,097  
 ; PRIOR FILING DATE: 1998-01-14  
 ; PRIOR APPLICATION NUMBER: 08/409,851  
 ; PRIOR FILING DATE: 1995-03-23  
 ; PRIOR APPLICATION NUMBER: 08/122,796  
 ; PRIOR FILING DATE: 1993-09-16  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 255  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-877-336-2

Query Match 82.7%; Score 115; DB 10; Length 255;  
 Best Local Similarity 80.0%; Pred. No. 4e-09;  
 Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
 DB 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 11  
 US-10-097-330-9  
 ; Sequence 9, Application US/10097330  
 ; Publication No. US20020127651A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ni et al.  
 ; TITLE OF INVENTION: HUMAN 4-1BB RECEPTOR SPLICING VARIANT  
 ; FILE REFERENCE: PF254D1C2  
 ; CURRENT APPLICATION NUMBER: US/10/097,330  
 ; CURRENT FILING DATE: 2002-03-15  
 ; PRIOR APPLICATION NUMBER: US 09/739,394  
 ; PRIOR FILING DATE: 2000-12-19  
 ; PRIOR APPLICATION NUMBER: US 09/253,549  
 ; PRIOR FILING DATE: 1999-02-22  
 ; PRIOR APPLICATION NUMBER: US 08/816,605  
 ; PRIOR FILING DATE: 1997-03-13  
 ; PRIOR APPLICATION NUMBER: US 60/013,474  
 ; PRIOR FILING DATE: 1996-03-15  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 9  
 ; LENGTH: 255  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-097-330-9

Query Match 82.7%; Score 115; DB 13; Length 255;  
 Best Local Similarity 80.0%; Pred. No. 4e-09;  
 Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
 DB 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 12  
 US-10-027-199-2  
 ; Sequence 2, Application US/10027199  
 ; Publication No. US20020168719A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kwon, Byoung  
 ; TITLE OF INVENTION: NEW RECEPTOR AND RELATED PRODUCTS AND  
 ; FILE REFERENCE: 740.013US2  
 ; CURRENT APPLICATION NUMBER: US/10/027,199  
 ; CURRENT FILING DATE: 2001-12-20  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/955,572  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-22  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/461,652  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1995-06-05  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/122,796  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1993-09-03  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 255  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-027-199-2

Query Match 82.7%; Score 115; DB 13; Length 255;  
 Best Local Similarity 80.0%; Pred. No. 4e-09;  
 Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
 DB 133 CRPWTNCSLDGKSVLVNGTKERDVV 157

RESULT 13  
 US-10-170-997-2

; Sequence 2, Application US/10170997  
; Publication No. US20030082157A1  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung Se  
; TITLE OF INVENTION: New Receptor and Related Products and Methods  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Barnard, Brown & Michaels  
; STREET: 306 East State Street, Suite 220  
; CITY: Ithaca  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 14850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/170,997  
; FILING DATE: 12-Jun-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/955,573  
; FILING DATE: 22-OCT-1997  
; APPLICATION NUMBER: 08/460,976  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/122,796  
; FILING DATE: 13-SEP-1993  
; APPLICATION NUMBER: US 08/012,269  
; FILING DATE: 01-FEB-1993  
; APPLICATION NUMBER: US 07/922,996  
; FILING DATE: 30-JUL-1992  
; APPLICATION NUMBER: US 08/267,577  
; FILING DATE: 07-NOV-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michaels, Christopher A  
; REGISTRATION NUMBER: 34,390  
; REFERENCE/DOCKET NUMBER: KWO4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 607-273-1711  
; TELEFAX: 607-273-2609  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 255 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-170-997-2  
  
Query Match 82.7%; Score 115; DB 14; Length 255;  
Best Local Similarity 80.0%; Pred. No. 4e-09;  
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
Db 133 CRPWTNCSLDGRSVLVNGTKERDVV 157  
  
RESULT 14  
US-10-186-643-11  
; Sequence 11, Application US/10186643  
; Publication No. US20030118546A1  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Ying-Fei  
; APPLICANT: Ni, Jian  
; APPLICANT: Gentz, Reiner  
; APPLICANT: Ruben, Steven  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
; FILE REFERENCE: 1488.1280004  
; CURRENT APPLICATION NUMBER: US/10/186,643

; CURRENT FILING DATE: 2002-07-02  
; PRIOR APPLICATION NUMBER: US/09/573,986  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-186-643-11  
  
Query Match 82.7%; Score 115; DB 14; Length 255;  
Best Local Similarity 80.0%; Pred. No. 4e-09;  
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
Db 133 CRPWTNCSLDGRSVLVNGTKERDVV 157  
  
RESULT 15  
US-10-207-655-160  
; Sequence 160, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; APPLICANT: Hayden-Ledbetter, Martha S.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 390069.401C1  
; CURRENT APPLICATION NUMBER: US/10/207,655  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 160  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-207-655-160  
  
Query Match 82.7%; Score 115; DB 14; Length 255;  
Best Local Similarity 80.0%; Pred. No. 4e-09;  
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
Db 133 CRPWTNCSLDGRSVLVNGTKERDVV 157  
  
RESULT 16  
US-10-418-242-13  
; Sequence 13, Application US/10418242  
; Publication No. US20040013664A1  
; GENERAL INFORMATION:  
; APPLICANT: Gentz et al.  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta  
; FILE REFERENCE: PF454P3  
; CURRENT APPLICATION NUMBER: US/10/418,242  
; CURRENT FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: 60/373,604  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: 09/935,727  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 60/303,224  
; PRIOR FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: 60/252,131  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: 60/227,598  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: 09/518,931  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: 60/168,235  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 60/146,371





;; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB  
;; NUMBER OF SEQUENCES: 19  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Immunex Corporation, Law Department  
;; STREET: 51 University Street  
;; CITY: Seattle  
;; STATE: WA  
;; COUNTRY: USA  
;; ZIP: 98101  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: Apple Power Macintosh  
;; OPERATING SYSTEM: Apple Operating System 7.5.5  
;; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/865,363  
;; FILING DATE: 25-May-2001  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/995,659  
;; FILING DATE: <Unknown>  
;; APPLICATION NUMBER: USN 08/813,509  
;; FILING DATE: 07 MARCH 1997  
;; APPLICATION NUMBER: USN 08/772,330  
;; FILING DATE: 23 DECEMBER 1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Perkins, Patricia Anne  
;; REGISTRATION NUMBER: 34,693  
;; REFERENCE/DOCKET NUMBER: 2852-A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206)587-0430  
;; TELEFAX: (206)233-0644  
;; INFORMATION FOR SEQ ID NO: 15:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 625 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-865-363-15

Query Match 61.9%; Score 86; DB 12; Length 625;  
Best Local Similarity 60.0%; Pred. No. 0.00026;  
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
|:|||||:|:|  
Db 170 CKPWTNCTLLGKLEAHQGTTESDVV 194

RESULT 20  
US-10-151-071-2  
; Sequence 2, Application US/10151071  
; Publication No. US2003001751A1  
; GENERAL INFORMATION:  
; APPLICANT: DOUGALL, William  
; APPLICANT: ANDERSON, Dirk  
; TITLE OF INVENTION: THERAPEUTIC USES OF RANK ANTAGONISTS  
; FILE REFERENCE: 3277-A  
; CURRENT APPLICATION NUMBER: US/10/151.071  
; CURRENT FILING DATE: 2001-05-17  
; PRIOR APPLICATION NUMBER: 60/291,919  
; PRIOR FILING DATE: 2001-05-17  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 625  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-151-071-2

Query Match 61.9%; Score 86; DB 12; Length 625;  
Best Local Similarity 60.0%; Pred. No. 0.00026;

Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
|:|||||:|:|  
Db 170 CKPWTNCTLLGKLEAHQGTTESDVV 194  
RESULT 21  
US-09-957-944-4  
; Sequence 4, Application US/09957944  
; Publication No. US20020086312A1  
; GENERAL INFORMATION:  
; APPLICANT: Dougall, William C.  
; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS AND ANTAGONISTS OF RECEPTOR ACTIVAT  
; FILE REFERENCE: 3109-A  
; CURRENT APPLICATION NUMBER: US/09/957,944  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/235,157  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 625  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-09-957-944-4

Query Match 61.9%; Score 86; DB 12; Length 625;  
Best Local Similarity 60.0%; Pred. No. 0.00026;  
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
|:|||||:|:|  
Db 170 CKPWTNCTLLGKLEAHQGTTESDVV 194

RESULT 22  
US-10-166-232A-2  
; Sequence 2, Application US/10166232A  
; Publication No. US20030021785A1  
; GENERAL INFORMATION:  
; APPLICANT: DOUGALL, William, C.  
; TITLE OF INVENTION: USE OF RANK ANTAGONISTS TO TREAT CANCER  
; FILE REFERENCE: 3278-A  
; CURRENT APPLICATION NUMBER: US/10/166,232A  
; CURRENT FILING DATE: 2002-06-05  
; PRIOR APPLICATION NUMBER: 60/296,670  
; PRIOR FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 625  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-166-232A-2

Query Match 61.9%; Score 86; DB 14; Length 625;  
Best Local Similarity 60.0%; Pred. No. 0.00026;  
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
|:|||||:|:|  
Db 170 CKPWTNCTLLGKLEAHQGTTESDVV 194

RESULT 23  
US-10-405-878-15  
; Sequence 15, Application US/10405878  
; Publication No. US20030175840A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Dirk M.  
; Galibert, Laurent

```

; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION NUMBER: US/10/405,878
; FILING DATE: 01-Apr-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-405-878-15

Query Match 61.9%; Score 86; DB 14; Length 625;
Best Local Similarity 60.0%; Pred. No. 0.00026;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTKDVV 25
DB 170 CKPWTNCTLLGKLEAHQGTTSDDV 194

RESULT 24
US-09-768-779A-2
; Sequence 2, Application US/09768779A
; Patent No. US20020127637A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; MOORE, PAUL
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/768,779A
; FILING DATE: 25-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/086,582
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: KENLEY K. HOOVER
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF368PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 615 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-768-779A-2

Query Match 56.8%; Score 79; DB 9; Length 615;
Best Local Similarity 56.0%; Pred. No. 0.0029;
Matches 14; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTKDVV 25
DB 168 CRPWTNCTFLGKRVHHGTEKSDVV 192

RESULT 25
US-10-291-480-2
; Sequence 2, Application US/10291480
; Publication No. US20030100069A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Moore, Paul
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Protein 8
; FILE REFERENCE: PF368CID1
; CURRENT APPLICATION NUMBER: US/10/291,480
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/768,779
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/086,582
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/048,020
; PRIOR FILING DATE: 1997-05-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 615
; TYPE: PRT
; ORGANISM: human
; US-10-291-480-2

Query Match 56.8%; Score 79; DB 14; Length 615;
Best Local Similarity 56.0%; Pred. No. 0.0029;
Matches 14; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTKDVV 25
DB 168 CRPWTNCTFLGKRVHHGTEKSDVV 192

RESULT 26
US-10-151-071-5
; Sequence 5, Application US/10151071
; Publication No. US20030017151A1
; GENERAL INFORMATION:

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STATE: USA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/877,650  
FILING DATE: 08-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/995,659  
FILING DATE: 1997-12-22  
APPLICATION NUMBER: USSN 08/813,509  
FILING DATE: 07 MARCH 1997  
APPLICATION NUMBER: USSN 08/772,330  
FILING DATE: 23 DECEMBER 1996  
ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2852-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 451 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-877-650-4

Query Match 54.0%; Score 75; DB 9; Length 451;  
Best Local Similarity 52.0%; Pred. No. 0.0083;  
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTETKDVV 25  
Db 169 CRPWTNCTFLGKRVHHGTEKSDAV 193

## RESULT 30

US-09-865-363-4

; Sequence 4, Application US/09865363

; Publication No. US2002008626A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/865,363

; FILING DATE: 25-May-2001

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/995,659

; FILING DATE: &lt;Unknown&gt;

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2852-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 451 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-865-363-4

Query Match 54.0%; Score 75; DB 12; Length 451;  
Best Local Similarity 52.0%; Pred. No. 0.0083;  
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTETKDVV 25  
Db 169 CRPWTNCTFLGKRVHHGTEKSDAV 193

## RESULT 31

US-10-405-878-4

; Sequence 4, Application US/10405878

; Publication No. US20030175840A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/405,878

; FILING DATE: 01-Apr-2003

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/996,139

; FILING DATE: 22 DECEMBER 1997

; APPLICATION NUMBER: USSN 60/064,671

; FILING DATE: 14 OCTOBER 1997

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2851-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 451 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-405-878-4

Query Match 54.0%; Score 75; DB 14; Length 451;  
Best Local Similarity 52.0%; Pred. No. 0.0083;  
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTETKDVV 25  
Db 169 CRPWTNCTFLGKRVHHGTEKSDAV 193

## RESULT 32

US-09-871-856-2

; Sequence 2, Application US/09871856

; Patent No. US20020081720A1

```

GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Maraskovsky, Eugene
Galibert, Laurent
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-871-856-2
Query Match 54.0%; Score 75; DB 9; Length 591;
Best Local Similarity 52.0%; Pred. No. 0.011;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 144 CRPWTNCTFLGKRVHHGTEKSDAV 168

RESULT 34
US-09-865-363-2
Sequence 2, Application US/09865363
Publication No. US20020086826A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,363
FILING DATE: 25-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:

GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-871-856-2
Query Match 54.0%; Score 75; DB 9; Length 591;
Best Local Similarity 52.0%; Pred. No. 0.011;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 144 CRPWTNCTFLGKRVHHGTEKSDAV 168

RESULT 33
US-09-877-650-2
Sequence 2, Application US/09877650
Patent No. US20020169117A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
```

```
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-865-363-2
Query Match 54.0%; Score 75; DB 12; Length 591;
Best Local Similarity 52.0%; Pred. No. 0.011;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 144 CRPWTNCTFLGKRVHGHGTEKSDAV 168

RESULT 35
US-10-405-878-2
; Sequence 2, Application US/10405878
; Publication No. US20030175840A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/405,878
; FILING DATE: 01-Apr-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
```

```
US-10-405-878-2
Query Match 54.0%; Score 75; DB 14; Length 591;
Best Local Similarity 52.0%; Pred. No. 0.011;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 144 CRPWTNCTFLGKRVHGHGTEKSDAV 168

RESULT 36
US-09-871-856-6
; Sequence 6, Application US/09871856
; Patent No. US20020081720A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,856
; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 616 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-871-856-6
Query Match 54.0%; Score 75; DB 9; Length 616;
Best Local Similarity 52.0%; Pred. No. 0.012;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 169 CRPWTNCTFLGKRVHGHGTEKSDAV 193

RESULT 37
US-09-877-650-6
; Sequence 6, Application US/09877650
; Patent No. US20020169117A1
```



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; GENERAL INFORMATION:
; APPLICANT: Dougall, William C.
; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS AND ANTAGONISTS OF RECEPTOR ACTIVATION
; TITLE OF INVENTION: NF-Kappa B
; FILE REFERENCE: 3109-A
; CURRENT APPLICATION NUMBER: US/09/957,944
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/235,157
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-957-944-2

Query Match          54.0%; Score 75; DB 12; Length 616;
Best Local Similarity 52.0%; Pred. No. 0.012;
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY      1 CRPTWNCSLDGRSVLKTGTTEKDVV 25
      |||||:|:|:|:|:|:|:|:|:|
Db      169 CRPTWNCITFLGKRVVHHGTEKSDAV 193

Search completed: May 5, 2004, 14:53:54
Job time : 10.2466 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2004, 14:34:41 ; Search time 2.99658 Seconds

(without alignments)  
802.512 Million cell updates/sec

Title: US-10-067-122b-2\_COPY\_133\_157

Perfect score: 139

Sequence: 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	256	2 B32393	T-cell antigen 4-1
2	115	82.7	255	2 I38426	lymphocyte activat
3	73	52.5	277	2 I37552	OX40 homolog - hum
4	70	50.4	271	2 I12783	OX40 antigen precu
5	66	47.5	272	2 I48700	gene ox40 protein
6	63	45.3	277	2 A60771	B-cell activation
7	62	44.6	305	2 A46476	B cell-associated
8	53.5	38.5	772	2 D75002	chemotaxis histidi
9	50	36.0	230	2 T47317	hypothetical prote
10	50	36.0	354	2 T47965	hypothetical prote
11	49.5	35.6	170	2 E96523	hypothetical prote
12	48.5	34.9	766	2 G71160	probable histidine
13	48	34.5	115	2 AD1172	hypothetical prote
14	48	34.5	175	2 S48280	probable membrane
15	48	34.5	194	2 S57472	murine muscle LIM
16	48	34.5	194	2 A55099	death receptor-6 -
17	48	34.5	651	2 JC7705	probable membrane
18	47.5	34.2	463	2 S19377	transposase sll198
19	47	33.8	119	2 S75117	transposase sll198
20	47	33.8	231	2 E97280	amidase, germinati
21	47	33.8	364	2 G82740	riboflavin-specifi
22	47	33.8	998	1 Q0BBB1	Bi protein A - black
23	47	33.8	998	2 S41397	protein A - flock
24	47	33.8	1127	2 T03105	major single-stran
25	46	33.1	254	1 COBQ02	cyclin homolog ECL
26	46	33.1	348	1 XDEC	asparaginase [EC 3
27	46	33.1	348	2 A98108	periplasmic L-aspa
28	46	33.1	348	2 D85953	periplasmic L-aspa
29	46	33.1	361	2 AF1593	B. subtilis PBSX p

## ALIGNMENTS

### RESULT 1

T-cell antigen 4-1BB precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 21-Jul-2000

C:Accession: B32393; I48879

R:Kwon, B.S.; Weissman, S.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989

A:Title: cDNA sequence of two inducible T-cell genes

A:Reference number: A32393; MUID:89184547; PMID:2784565

A:Accession: B32393

A:Molecule type: mRNA

A:Residues: 1-256 <KWO>

A:Cross-references: GB:J04492; NID:9201121; PIDN:AAA40167.1; PID:9201122

R:Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.

J. Immunol. 152, 2256-2262, 1994

A:Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1BB.

A:Reference number: I48879; MUID:94179805; PMID:8133039

A:Accession: I48879

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-256 <RES>

A:Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178

C:Genetics:

A:Introns: 35/1; 69/1; 115/1; 139/2; 156/3; 181/1; 225/1

C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: transmembrane protein

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 100.0%; Score 139; DB 2; Length 256;

Best Local Similarity 100.0%; Pred. No. 3.1e-13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25

DB 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

### RESULT 2

I38426

lymphocyte activation-induced receptor ILA precursor - human

C:Species: Homo sapiens (man)

C>Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 01-Dec-2000

C:Accession: I38426; J070752

R:Ralderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; R.

Eur. J. Immunol. 24, 2219-2227, 1994

A:Title: Molecular and biological characterization of human 4-1BB and its ligand.

A:Reference number: I38426; MUID:94374434; PMID:8088337

A:Accession: I38426

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA



D75002  
chemotaxis histidine kinase (cheA) PAB1332 - Pyrococcus abyssi (strain Orsay)  
C;Species: Pyrococcus abyssi  
C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000  
C;Accession: D75002  
R;anonymous, Genoscope



RESULT 15  
S57472  
murine muscle LIM protein - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 10-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 15-Jun-2001  
C:Accession: S57472  
R:Harrod, G.V.; Jowett, A.K.  
submitted to the EMBL Data Library, June 1995  
A:Description: Murine MLP: cloning and expression in the embryonic head.  
A:Reference number: S57472  
A:Accession: S57472  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-194 <HAR>  
A:Cross-references: EMBL:Z49883; NID:g871430; PIDN:CAA90039.1; PID:g871431  
C:Superfamily: mouse muscle LIM protein MLP; LIM metal-binding repeat homology  
F:10-61/Domain: LIM metal-binding repeat homology <LIM1>  
F:120-171/Domain: LIM metal-binding repeat homology <LIM2>  
  
Query Match 34.5%; Score 48; DB 2; Length 194;  
Best Local Similarity 34.6%; Pred. No. 12;  
Matches 9; Conservative 6; Mismatches 7; Indels 4; Gaps 1;  
  
QY 2 RPW-----TNCSDGRSVLKTGTTEKD 23  
Db 138 KPWKTCFRCACGKSLSTNVTDKD 163  
  
RESULT 16  
A55099  
muscle LIM protein - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 15-Jun-2001  
C:Accession: A55099  
R:Arber, S.; Halder, G.; Caroni, P.  
Cell 79, 221-231, 1994  
A>Title: Muscle LIM protein, a novel essential regulator of myogenesis, promotes myogeni  
A:Reference number: A55099; MUID:95042720; PMID:7954791  
A:Accession: A55099  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-194 <RES>  
A:Cross-references: EMBL:X81193; NID:g535068; PIDN:CAA57065.1; PID:g535069  
C:Genetics:  
A:Gene: MLP  
C:Superfamily: mouse muscle LIM protein MLP; LIM metal-binding repeat homology  
F:10-61/Domain: LIM metal-binding repeat homology <LIM1>  
F:120-171/Domain: LIM metal-binding repeat homology <LIM2>  
  
Query Match 34.5%; Score 48; DB 2; Length 194;  
Best Local Similarity 34.6%; Pred. No. 12;  
Matches 9; Conservative 6; Mismatches 7; Indels 4; Gaps 1;  
  
QY 2 RPWTN-----CSLDGRSVLKTGTTEKD 23  
Db 138 KPWKTCFPCACGKSLSTNVTDKD 163  
  
RESULT 17  
JC7705  
death receptor-6 - chicken  
C:Species: Gallus gallus (chicken)  
C>Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 07-Jul-2003  
C:Accession: JC7705  
R:Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.  
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001  
A>Title: Conservation of death receptor-6 in avian and piscine vertebrates.  
A:Reference number: JC7705; MUID:21308433; PMID:11414698  
A:Accession: JC7705  
A:Molecule type: mRNA  
A:Residues: 1-651 <BRI>  
A:Cross-references: GB:AF349908  
C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs

tresia, activates a cell death and/or survival signaling cascade.  
C:Genetics:  
A:Gene: dr-6  
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C:Keywords: ovary  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>  
F:332-350/Domain: transmembrane #status predicted <TM>  
F:410-475/Domain: death domain #status predicted <DED>  
F:551-651/Region: conserved cytoplasmic #status predicted  
  
Query Match 34.5%; Score 48; DB 2; Length 651;  
Best Local Similarity 40.0%; Pred. No. 40;  
Matches 10; Conservative 4; Mismatches 11; Indels 0; Gaps 0;  
  
QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
Db 171 CKTYDCFGKMMVVVKPTKESDNV 195  
  
RESULT 18  
S19377  
probable membrane protein YCL048w - yeast (Saccharomyces cerevisiae)  
C:Species: Saccharomyces cerevisiae  
C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 19-Apr-2002  
C:Accession: S19377  
R:Grenson, M.; Jauniaux, J.C.; Urrestarazu, L.A.  
submitted to the Protein Sequence Database, March 1992  
A:Reference number: S19376  
A:Accession: S19377  
A:Molecule type: DNA  
A:Residues: 1-463 <GRB>  
A:Cross-references: EMBL:X59720; NID:gl907116; PID:g5313; GSPDB:GN00003; MIPS:YCL048w  
C:Genetics:  
A:Gene: MIPS:YCL048w  
A:Cross-references: SGD:S0000553  
A:Map position: 3L  
C:Keywords: transmembrane protein  
F:7-29/Domain: transmembrane #status predicted <TM1>  
F:446-463/Domain: transmembrane #status predicted <TM2>  
  
Query Match 34.2%; Score 47.5; DB 2; Length 463;  
Best Local Similarity 50.0%; Pred. No. 34;  
Matches 9; Conservative 4; Mismatches 4; Indels 1; Gaps 1;  
  
QY 1 CRPWTNCSLDGRSVLKTG 18  
Db 378 CNKWTNPS-NGRSIRGG 394  
  
RESULT 19  
S15117  
transposase sl11985 - Synchocystis sp. (strain PCC 6803)  
N:Alternate names: protein sl11985  
C:Species: Synchocystis sp.  
A:Variety: PCC 6803  
C>Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 15-Oct-1999  
C:Accession: S75117  
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
DNA Res. 3, 109-136, 1996  
A>Title: Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis  
s.  
A:Reference number: S74322; MUID:97061201; PMID:8905231  
A:Accession: S75117  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-119 <KAN>  
A:Cross-references: EMBL:D90910; GB:AB001339; NID:gl652956; PIDN:BAAL17979.1; PID:dl01871.  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Keywords: DNA binding; DNA recombination  
  
Query Match 33.8%; Score 47; DB 2; Length 119;

Best Local Similarity 50.0%; Pred. No. 9.9;  
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 RPWTNCSLDGRSVLKT 17  
|||||:|||||:  
Db 104 RPWNQKVDGKTYLTT 119

## RESULT 20

E97280  
amidase, germination specific (cwlC/cwID B. subtilis ortholog) [imported] - Clostridium  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
C:Accession: E97280  
R: Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: E97280  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-231 <KUR>  
A:Cross-references: GB:AB001437; PIDN:AAK61032.1; PID:q15026157; GSPDB:GN00168  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC3092

Query Match 33.8%; Score 47; DB 2; Length 231;  
Best Local Similarity 56.2%; Pred. No. 20;  
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 9 LDGRSVLKTGTEDV 24  
:||||:|||||:  
Db 50 IDGGANLKDGTLEKDI 65

## RESULT 21

G82740  
riboflavin-specific deaminase XF0950 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Sep-2000  
C:Accession: G82740  
R: Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717; PMID:10910347  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: G82740  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-364 <SIM>  
A:Cross-references: GB:AB003934; GB:AE003849; NID:G9105876; PIDN:AAF83760.1; GSPDB:GN001  
A:Experimental source: strain 9a5c  
R: Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H  
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Tshukano, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF0950  
C:Superfamily: Chlamydophila pneumoniae riboflavin-specific deaminase

Query Match 33.8%; Score 47; DB 2; Length 364;

Best Local Similarity 41.7%; Pred. No. 31;  
Matches 10; Conservative 4; Mismatches 6; Indels 4; Gaps 1;

QY 2 RPWT----NCSLDGRSVLKTGTTE 21  
|||||:|||||:  
Db 151 RPWRIKLGSSLDGRTALASGESK 174

## RESULT 22

Q088B1  
B1 protein - black beetle virus  
C:Species: black beetle virus  
C:Date: 30-Sep-1992 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999  
C:Accession: S78471; S28728; S28729; A23243  
R: Dasgupta, R.  
submitted to the EMBL Data Library, July 1986  
A:Reference number: S78471  
A:Molecule type: genomic RNA  
A:Residues: 1-998 <DAS>  
A:Cross-references: EMBL:X02396; NID:G60679; PIDN:CAA26238.1; PID:G60680  
R: Dasmahapatra, B.; Dasgupta, R.; Ghosh, A.; Kaesberg, P.  
J. Mol. Biol. 182, 183-189, 1985  
A:Title: Structure of the black beetle virus genome and its functional implications.  
A:Reference number: S28728; MUID:85210903; PMID:3839022  
A:Accession: S28728  
A:Molecule type: genomic RNA  
A:Residues: 1-883; 'AALRTPTWTRVQC' <DAW>  
A:Cross-references: EMBL:X02396  
A:Accession: S28729  
A:Molecule type: genomic RNA  
A:Residues: 897-998 <DA2>  
A:Cross-references: EMBL:X02396  
R: Guarino, L.A.; Ghosh, A.; Dasmahapatra, B.; Dasgupta, R.; Kaesberg, P.  
Virology 139, 139-203, 1984  
A:Title: Sequence of the black beetle virus subgenomic RNA and its location in the viral  
A:Reference number: A23243; MUID:85042104; PMID:6495657  
A:Accession: A23243  
A:Molecule type: genomic RNA  
A:Residues: 897-998 <GUA>  
A:Cross-references: GB:M33065; NID:G210673; PIDN:AAA42745.1; PID:G210674  
C:Superfamily: black beetle virus B1 protein  
C:Keywords: RNA biosynthesis

Query Match 33.8%; Score 47; DB 1; Length 998;

Best Local Similarity 85.7%; Pred. No. 88;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNC 7  
|||||:  
Db 262 CRPWTDC 268

## RESULT 23

S41397  
protein A - flock house virus  
C:Species: flock house virus  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 11-Jan-2000  
C:Accession: S41397  
R: Dasgupta, R.  
submitted to the EMBL Data Library, January 1994  
A:Description: Near identity in the polymerase gene of two serologically distinct nodavir  
A:Reference number: S41397  
A:Accession: S41397  
A:Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-998 <DAS>  
A:Cross-references: EMBL:X77156; NID:G450500; PIDN:CAA54399.1; PID:G450501  
C:Superfamily: black beetle virus B1 protein

Query Match 33.8%; Score 47; DB 2; Length 998;

Best Local Similarity 85.7%; Pred. No. 88;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNC 7  
|||||:  
Db 262 CRPWTDC 268

## RESULT 23

S41397  
protein A - flock house virus  
C:Species: flock house virus  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 11-Jan-2000  
C:Accession: S41397  
R: Dasgupta, R.  
submitted to the EMBL Data Library, January 1994  
A:Description: Near identity in the polymerase gene of two serologically distinct nodavir  
A:Reference number: S41397  
A:Accession: S41397  
A:Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-998 <DAS>  
A:Cross-references: EMBL:X77156; NID:G450500; PIDN:CAA54399.1; PID:G450501  
C:Superfamily: black beetle virus B1 protein

Query Match 33.8%; Score 47; DB 2; Length 998;

Best Local Similarity 85.7%; Pred. No. 88;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNC 7  
Db 262 CREWTDG 268

RESULT 24  
T03105  
Major single-stranded DNA binding protein - alcelaphine herpesvirus 1  
C:Species: alcelaphine herpesvirus 1  
C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 24-Nov-1999  
C:Accession: T03105  
J:Ensser, A.; Pfanz, R.; Fleckenstein, B.  
J. Virol. 71, 6517-6525, 1997  
A:Title: Primary structure of the alcelaphine herpesvirus 1 genome.  
A:Reference number: Z14840; MUID:97404659; PMID:9261371  
A:Accession: T03105  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-1127 <ENS>  
A:Cross-references: EMBL:AF005370; NID:92337967; PIDN:AA058057.1; PID:92337973  
C:Superfamily: herpesvirus DNA-binding protein  
C:Keywords: DNA binding

Query Match 33.8%; Score 47; DB 2; Length 1127;  
Best Local Similarity 52.2%; Pred. No. 1e+02;  
Matches 12; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY 3 PWTNCSLDGRSVLKTGTTEKDVV 25  
Db 1069 PWTHEWAB--SVLKSGTCETDEV 1089

RESULT 25  
COR02  
Cyclin homolog ECLF2 - saimirine herpesvirus 1 (strain 11)  
C:Species: saimirine herpesvirus 1  
A:Note: host Saimiri sciureus (common squirrel monkey)  
C:Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 18-Jun-1999  
C:Accession: S20243; F36813  
R:Nicholas, J.; Cameron, K.R.; Honess, R.W.  
Nature 355, 362-365, 1992  
A:Title: Herpesvirus saimiri encodes homologues of G protein-coupled receptors and cyclin  
A:Reference number: S20243; MUID:92115001; PMID:1309943  
A:Accession: S20243  
A:Molecule type: DNA  
A:Residues: 1-254 <NIC>  
A:Cross-references: GB:S76368; NID:92433351; PIDN:AAB21115.1; PID:92433352  
R:Albrecht, J.  
submitted to the EMBL Data Library, January 1992  
A:Description: Primary structure of the herpesvirus saimiri genome.  
A:Reference number: A36806  
A:Accession: F36813  
A:Molecule type: DNA  
A:Residues: 1-254 <ALB>  
A:Cross-references: GB:X64346; NID:950320; PIDN:CAA45695.1; PID:960393  
R:Albrecht, J.C.; Nicholas, J.; Baller, D.; Cameron, K.R.; Biesinger, B.; Newman, C.; Wi  
J. Virol. 66, 5047-5058, 1992  
A:Title: Primary structure of the herpesvirus saimiri genome.  
A:Reference number: A37309; MUID:92333688; PMID:1321287  
A:Contents: annotation; possible protein-coding frames  
A:Note: neither amino acid nor nucleotide sequence is given  
C:Genetics:  
A:Gene: ECLF2; 72  
C:Superfamily: cyclin  
C:Keywords: cell cycle control

Query Match 33.1%; Score 46; DB 1; Length 254;  
Best Local Similarity 44.8%; Pred. No. 31;  
Matches 13; Conservative 1; Mismatches 11; Indels 4; Gaps 1;

QY 1 CRPWTNCSLDGRSVLKTGT-----TEKDVV 25  
Db 1069 PWTHEWAB--SVLKSGTCETDEV 1089

Db 214 CRPWTCTCYLEDLSSILNFTNTVTRTKDQV 242

## RESULT 26

XDEC

asparaginase (EC 3.5.1.1) II precursor [validated] - Escherichia coli (strain K-12)  
C:Species: Escherichia coli  
C:Date: 24-Apr-1984 #sequence\_revision 31-Dec-1990 #text\_change 01-Mar-2002  
C:Accession: A35132; J03031; A01000; D65081  
R:Jennings, M.F.; Beacham, I.R.  
J. Bacteriol. 172, 1491-1498, 1990  
A:Title: Analysis of the Escherichia coli gene encoding L-asparaginase II, ansB, and its  
A:Reference number: A35132; MUID:90170867; PMID:2407723  
A:Accession: A35132  
A:Molecule type: DNA  
A:Residues: 1-348 <JEN>  
A:Cross-references: EMBL:X52540  
R:Bonthron, D.T.  
Gene 91, 101-105, 1990  
A:Title: L-Asparaginase II of Escherichia coli K-12: cloning, mapping and sequencing of t  
A:Reference number: J03031; MUID:90382683; PMID:2144836  
A:Accession: J03031  
A:Molecule type: DNA  
A:Residues: 1-348 <SON>  
A:Cross-references: GB:M34234; NID:9145276; PIDN:AAA23445.1; PID:9145277  
A:Experimental source: strain K12 JM108  
R:Maita, T.; Matsuda, G.  
Hoppe-Seyler's Z. Physiol. Chem. 361, 105-117, 1980  
A:Title: The primary structure of L-asparaginase from Escherichia coli.  
A:Reference number: A01000; MUID:80135739; PMID:6766894  
A:Accession: A01000  
A:Molecule type: protein  
A:Residues: 23-48, 'A', 50-85, 'D', 87-131, 133-155, 157-170, 172-205, 'D', 207-267, 'D', 269-273, 'J  
R:Peterson, R.G.; Richards, F.F.; Handschumacher, R.E.  
J. Biol. Chem. 252, 2072-2076, 1977  
A:Title: Structure of peptide from active site region of Escherichia coli L-asparaginase  
A:Reference number: A32655; MUID:77140944; PMID:321449  
A:Contents: annotation; active site  
R:Greenquist, A.C.; Wriston Jr., J.C.  
Arch. Biochem. Biophys. 152, 280-286, 1972  
A:Title: Chemical evidence for identical subunits in L-asparaginase from Escherichia coli  
A:Reference number: A37451; MUID:73007901; PMID:4561256  
A:Contents: annotation  
A:Note: the cysteine residues were quantitated and shown to form intrachain bonds  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: D65081  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-348 <BLAT>  
A:Cross-references: GB:AB000378; GB:U00096; NID:91789319; PIDN:AA075994.1; PID:91789327;  
A:Experimental source: strain K-12, substrain MG1655  
C:Genetics:  
A:Gene: ansB  
A:Map position: 64 min  
C:Complex: homotetramer  
C:Function:  
A:Description: EC 3.5.1.1 [validated, MUID:90170867]; catalyzes the hydrolysis of aspara  
A:Note: has a higher affinity for asparagine than asparaginase I (PIR:XDECI)  
A:Note: positively regulated by cAMP receptor protein (CRP) (PIR:QRECC) and by FNR protei  
C:Superfamily: asparaginase  
C:Keywords: extracellular protein; homotetramer; hydrolase  
F1-22/Domain: signal sequence #status predicted <SIG>  
F23-348/Product: asparaginase #status experimental  
F99-127/Disulfide bonds: #status experimental  
F142/Active site: Ser #status experimental

Query Match 33.1%; Score 46; DB 1; Length 348;  
Best Local Similarity 69.2%; Pred. No. 42;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

QY 9 LDGRSVLKTGTTTE 21
    |||||
Db 177 LDGRDVTNTNTD 189

RESULT 27
A:98108
C:periplasmic L-asparaginase II [imported] - Escherichia coli (strain O157:H7, substrain R
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: A98108
R:Havashita, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: A98108
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-348 <HAV>
A:Cross-references: GB:BA000007; PIDN:BAB37256.1; PID:gl3363305; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 050952
C:Genetics:
A:Gene: ECS3833
C:Superfamily: asparaginase

    Query Match 33.1%; Score 46; DB 2; Length 348;
    Best Local Similarity 69.2%; Pred. No. 42;
    Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 LDGRSVLKTGTTTE 21
    |||||
Db 177 LDGRDVTNTNTD 189

RESULT 28
A:98593
C:periplasmic L-asparaginase II [imported] - Escherichia coli (strain O157:H7, substrain H
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: D85953
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: D85953
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-348 <STO>
A:Cross-references: GB:A8005174; NID:gl2517506; PIDN:AAG58088.1; GSPDB:GN00145; UWGP:Z43
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: ansB
C:Superfamily: asparaginase

    Query Match 33.1%; Score 46; DB 2; Length 348;
    Best Local Similarity 69.2%; Pred. No. 42;
    Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 LDGRSVLKTGTTTE 21
    |||||
Db 177 LDGRDVTNTNTD 189

RESULT 29
A:AF1593
B. subtilis PBX prophage protein homolog lin1287 [imported] - Listeria innocua (strain
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AF1593
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker

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; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AF1593
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-361 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC96518.1; PID:gl6413760; GSPDB:GN00178
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: lin1287

    Query Match 33.1%; Score 46; DB 2; Length 361;
    Best Local Similarity 36.4%; Pred. No. 44;
    Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 4 WTNCSLDGRSVLKTGTTTEKDVV 25
    |||||
Db 268 WKTINISGLVLRGKSVNDVI 289

RESULT 30
A:86917
C:probable monooxygenase [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: A86917
R:Coile, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: A86917
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-494 <STO>
A:Cross-references: GB:AL450380; NID:gl3092457; PIDN:CAC29573.1; GSPDB:GN00147
C:Genetics:
A:Gene: ML0065

    Query Match 33.1%; Score 46; DB 2; Length 494;
    Best Local Similarity 47.1%; Pred. No. 61;
    Matches 8; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 2 RPWTNCS--LDGRSVLK 16
    |||||
Db 72 RPWTRQAIADGKPILE 88

RESULT 31
A:T02123
C:hypothetical protein At2g40960 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T20B5.16; hypothetical protein T3K9.27
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 02-Feb-2001
C:Accession: T00760; T02123; A84836
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
submitted to the EMBL data library, November 1997
A:Description: Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence.
A:Reference number: Z14159
A:Accession: T00760
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-249 <ROI>
A:Cross-references: EMBL:AC002409; NID:g2623294; PID:g2623310
A:Experimental source: cultivar Columbia
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S

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submitted to the EMBL Data Library, February 1999  
 A;Description: Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence.  
 A;Reference number: Z14570  
 A;Accession: T02123  
 A;Status: translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-249 <ROW>  
 A;Cross-references: EMBL:AC004261; NID:G3402695; PID:G3402721  
 A;Experimental source: cultivar Columbia  
 R;lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VarAken, S.E.; Umayam, L.; Tallon, L.;  
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
 Nature 402, 761-768, 1999  
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A;Reference number: A84420; MUID:20083487; PMID:10617197  
 A;Accession: A84836  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-249 <STO>  
 A;Cross-references: GB:AE002093; NID:G2623310; PIDN:AA86456.1; GSPDB:GN00139  
 C;Genetics:  
 A;Gene: At2g40960; T20B5.16; T3K9.27  
 A;Map position: 2  
 A;Introns: 38/1

Query Match 32.7%; Score 45.5; DB 2; Length 249;  
 Best Local Similarity 50.8%; Pred. No. 36;  
 Matches 12; Conservative 0; Mismatches 9; Indels 3; Gaps 2;

QY 3 PW-TNC--SLDGRSVLKTGTETXD 23  
 |||||  
 DB 186 PWRVNCSSRDENVLKNNGNEAD 209

RESULT 32  
 KIFXMG  
 homoserine kinase (EC 2.7.1.39) - Corynebacterium glutamicum  
 C;Species: Corynebacterium glutamicum  
 C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Jun-1999  
 C;Accession: S00866; S18263; S07385  
 R;Peoples, O.P.; Liebl, W.; Bodis, M.; Maeng, P.J.; Follettie, M.T.; Archer, J.A.; Sinsk  
 Mol. Microbiol. 2, 63-72, 1988  
 A;Title: Nucleotide sequence and fine structural analysis of the Corynebacterium glutami  
 A;Reference number: S00865; MUID:88216182; PMID:2835591  
 A;Accession: S00866  
 A;Molecule type: DNA  
 A;Residues: 1-309 <PRO>  
 A;Cross-references: EMBL:Y00546; NID:G40502; PIDN:CAA68615.1; PID:G40504  
 A;Accession: S18261  
 A;Molecule type: protein  
 A;Residues: 2-11 <PRO2>  
 R;Mateos, L.M.; del Real, G.; Aguilar, A.; Martin, J.F.  
 Nucleic Acids Res. 15, 3922, 1987  
 A;Title: Nucleotide sequence of the homoserine kinase (thr B) gene of Brevibacterium lac  
 A;Reference number: S07385; MUID:87231082; PMID:3035505  
 A;Accession: S07385  
 A;Molecule type: DNA  
 A;Residues: 1-245, 'V', 247-309 <MATE>  
 A;Cross-references: EMBL:Y00140; NID:G39587; PIDN:CAA68332.1; PID:G39588  
 A;Note: the source is designated as Brevibacterium lactofermentum  
 C;Genetics:  
 A;Gene: thrB  
 C;Superfamily: homoserine kinase  
 C;Keywords: ATP; phosphotransferase  
 P;2-309/Product: homoserine kinase #status experimental <MATE>

Query Match 32.4%; Score 45; DB 1; Length 309;  
 Best Local Similarity 70.0%; Pred. No. 53;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WTNCSLDGRS 13  
 |||||  
 DB 153 WTNLSIDGKS 162

# RESULT 33

E90436  
 coA-ligase / coenzyme F390 synthetase, probable [imported] - Sulfolobus solfataricus  
 C;Species: Sulfolobus solfataricus  
 C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001  
 R;Shee, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-y  
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.  
 arett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
 submitted to GenBank, April 2001  
 A;Description: Sulfolobus solfataricus complete genome.  
 A;Reference number: A99139  
 A;Accession: E90436  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-339 <KUR>  
 A;Cross-references: GB:AE006641; NID:G13815936; PIDN:AAK42748.1; GSPDB:GN00155  
 C;Genetics:  
 A;Gene: SSO2627

Query Match 32.4%; Score 45; DB 2; Length 339;  
 Best Local Similarity 45.5%; Pred. No. 58;  
 Matches 10; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY 4 WTNCSLDGRSVLKTGTETKDVV 25  
 |||||  
 DB 22 WT--SLVARSILVTAQVTKNDIV 41

# RESULT 34

AE2425  
 hypothetical protein alr4957 [imported] - Nostoc sp. (strain PCC 7120)  
 C;Species: Nostoc sp. PCC 7120  
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
 C;Accession: AE2425  
 R;Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,  
 Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S  
 DNA Res. 8, 205-213, 2001  
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
 A;Reference number: AB1807; MUID:21595285; PMID:11759840  
 A;Accession: AE2425  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-358 <KUR>  
 A;Cross-references: GB:BA000019; PIDN:BA076556.1; PID:G17134095; GSPDB:GN00179  
 A;Experimental source: strain PCC 7120  
 C;Genetics:  
 A;Gene: alr4957  
 C;Superfamily: conserved hypothetical protein yacL

Query Match 32.4%; Score 45; DB 2; Length 358;  
 Best Local Similarity 39.1%; Pred. No. 62;  
 Matches 9; Conservative 7; Mismatches 5; Indels 2; Gaps 1;

QY 5 TNCSLDGR--SVLKTGTETKDVV 25  
 |||||  
 DB 165 TSCIIDGRIEALLTGFLEGGII 187

# RESULT 35

T23385  
 hypothetical protein K07A1.11 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Jan-2000  
 C;Accession: T23385  
 R;Percy, C.  
 submitted to the EMBL Data Library, October 1996  
 A;Reference number: Z19734  
 A;Accession: T23385  
 A;Status: preliminary; translated from GB/EMBL/DDBJ

QY 5 TNCNCSLDGRSVLTGTTKDV 24  
:  
|||:  
DB 61 SNLSMDAMQYFQAGVTQXDV 80

RESULT 38  
T23298  
hypothetical protein K04B12.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T23298  
R:Steward, C.  
submitted to the EMBL Data Library, December 1996  
A:Reference number: Z19723  
A:Accession: T23298  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-1806 <WIL>  
A:Cross-references: EMBL:Z83232; PIDN: CAB05755.1; GSPDF:GN00020; CESP:K04B12.1  
A:Experimental source: c.lone K04B12  
C:Genetics:  
A:Gene: CESP:K04B12.1  
A:Map position: 2  
A:Introns: 24/2; 77/3; 294/2; 378/3; 433/3; 478/3; 523/3; 743/1; 794/3; 1049/3; 1414/3; 1;

Query Match 32.4%; Score 45; DB 2; Length 1806;  
Best Local Similarity 64.3%; Pred. No. 3.3e+02;  
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 3 PWTNCSLDGRSVLK 16  
:  
|||:  
DB 109 PW--CSADGKSCLK 120

RESULT 39  
D70732  
hypothetical protein Rv2288 - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C:Accession: D70732  
R:R.Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998  
A:Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Accession: D70732  
A:Molecule type: DNA  
A:Residues: 1-125 <COL>  
A:Cross-references: GB:Z77163; GB:AL123456; NID:g3261610; PIDN: CAB00980.1; PID:g1449332  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: RV2288  
C:Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2288

Query Match 31.7%; Score 44; DB 2; Length 125;  
Best Local Similarity 33.3%; Pred. No. 30;  
Matches 9; Conservative 7; Mismatches 7; Indels 4; Gaps 1;

QY 2 RPWTNCSLDGRSVL----KTGTTKDV 24  
:  
|||:  
DB 46 RRWCDDVDGRKLLPPARRTGTOORRI 72

RESULT 40  
F81433  
probable heme-binding lipoprotein Cj0158c [imported] - Campylobacter jejuni (strain NCTC)  
C:Species: Campylobacter jejuni  
C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 03-Jun-2002  
C:Accession: F81433

R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling  
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell  
Nature 403, 665-668, 2000  
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp  
A;Reference number: A81250; MUID:20150912; PMID:10688204  
A;Accession: F81433  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-141 <PAR>  
A;Cross-references: GB:AL1139074; GB:AL111169; NID:g6967505; PIDN:CAB72642.1; PID:g696769  
A;Experimental source: serotype O2, strain NCTC 11168  
C;Genetics:  
A;Gene: Cj0158c  
C;Superfamily: Campylobacter jejuni probable heme-binding lipoprotein Cj0158c  
Query Match 31.7%; Score 44; DB 2; Length 141;  
Best Local Similarity 42.1%; Pred. No. 33;  
Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;  
QY 7 CSLDGRSVLKTGTTEKDVV 25  
Db 20 CSNDEKNISKNTQNTDQEVV 38  
|||:::| |:::|  
|||:::| |:::|

Search completed: May 5, 2004, 14:41:22  
Job time : 3.99658 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:30:56 ; Search time 1.96918 Seconds  
(without alignments)  
661.065 Million cell updates/sec

Title: us-10-067-122b-2\_copy\_133\_157  
Perfect score: 139  
Sequence: 1 CRPWTNCSLDGRSVLKTGTTEXDVV 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139	100.0	256	1 TNR9 MOUSE	P20334 mus musculu
2	115	82.7	255	1 TNR3 HUMAN	Q07011 homo sapien
3	86	61.9	625	1 TR11 MOUSE	O35305 mus musculu
4	75	54.0	616	1 TR11 HUMAN	Q9y6q6 homo sapien
5	73	52.5	277	1 TNR4 HUMAN	P43489 homo sapien
6	70	50.4	271	1 TNR4 RAT	P15725 rattus norv
7	66	47.5	272	1 TNR4 MOUSE	P47741 mus musculu
8	63	45.3	277	1 TNR5 HUMAN	P25942 homo sapien
9	62	44.6	289	1 TNR5 MOUSE	P27512 mus musculu
10	53.5	38.5	1179	1 EXS8 BUCAP	Q8X9A9 buchnera ep
11	52	37.4	269	1 TNR5 BOVIN	Q28203 bos taurus
12	50	36.0	655	1 TR21 HUMAN	O75509 homo sapien
13	49	35.3	430	1 TRLT MACFA	Q9n092 macaca fasc
14	48	34.5	175	1 YBM6 YEAST	P18268 saccharomyc
15	48	34.5	194	1 CSR3 HUMAN	P50461 homo sapien
16	48	34.5	134	1 CSR3 MOUSE	P50462 mus musculu
17	48	34.5	194	1 CSR3 RAT	P50463 rattus norv
18	48	34.5	228	1 TR18 MOUSE	O35714 mus musculu
19	47.5	34.2	463	1 YCE8 YEAST	P25380 saccharomyc
20	47	33.8	415	1 TNR3 MOUSE	P50284 mus musculu
21	47	33.8	998	1 RRPO BBV	Q96631 black beetl
22	47	33.8	998	1 RRPO BOOLV	Q292J0 boolaria vi
23	47	33.8	998	1 RRPO FHV	Q66529 flock house
24	46	33.1	241	1 TR18 HUMAN	Q9y5us homo sapien
25	46	33.1	254	1 CGH2 HSVSA	O01043 herpesviru
26	46	33.1	348	1 ASG2 ECOLI	P00805 escherichia
27	45	32.4	308	1 KHSE CORGL	Q07128 corynebacte
28	45	32.4	401	1 T11B HUMAN	O00300 homo sapien
29	45	32.4	401	1 T11B RAT	O08727 rattus norv
30	45	32.4	412	1 REA1 CAEEL	P90917 caenorhabdi
31	45	32.4	655	1 TR21 MOUSE	Q9epus mus musculu
32	44	31.7	125	1 YM88 MYCTU	Q50677 mycobacteri
33	44	31.7	357	1 WN9B HUMAN	O14905 homo sapien

#### ALIGNMENTS

##### RESULT 1

ID	TNR9 MOUSE	STANDARD;	PRT;	256 AA.
AC	P20334:			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB ligand receptor) (T-cell antigen 4-1BB) (CD137 antigen).			
DE	TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.			
GN	Mus musculus (Mouse).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89184547; PubMed=2784565;			
RA	Kwon B.S., Weissman S.M.;			
RT	"CDNA sequences of two inducible T-cell genes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALE/c;			
RX	MEDLINE=94179805; PubMed=8133039;			
RA	Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;			
RT	"Genomic organization and chromosomal localization of the T-cell antigen 4-1BB.";			
RL	J. Immunol. 152:2256-2262(1994).			
RN	[3]			
RP	CHARACTERIZATION, AND SEQUENCE OF 25-29.			
RX	MEDLINE=93139510; PubMed=7678621;			
RA	Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.,			
RT	"Inducible T cell antigen 4-1BB. Analysis of expression and function.";			
RL	J. Immunol. 150:771-781(1993).			
CC	-!- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T cell activation.			
CC	-!- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.			
CC	ASSOCIATES WITH P56-LCK. Interacts with TRAF1, TRAF2 AND TRAF3 (By similarity).			
CC	-!- SURCELLULAR LOCATION: Type I membrane protein.			
CC	-!- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.			
CC	-!- INDUCTION: Optimal by PMA and ionomycin.			
CC	-!- SIMILARITY: Contains 4 TNFR-Cys repeats.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified by this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; J04492; AAA40167.1; -			
DR	EMBL; U02567; AAA93113.1; -			

34 44 31.7 364 1 LEU3\_BUCUE Q9evh5 buchnera ap  
35 44 31.7 660 1 SCAG\_XENLA P51171 xenopus lae  
36 44 31.7 766 1 DAB2\_MOUSE P98078 mus musculu  
37 44 31.7 768 1 DAB2\_RAT O88797 rattus norv  
38 44 31.7 770 1 DAB2\_HUMAN P98082 homo sapien  
39 44 31.7 1582 1 YU30\_RALSO O8xv02 ralstonia s  
40 43.5 31.3 227 1 VGHG\_ECOLI P46846 escherichia  
41 43.5 31.3 294 1 AROK\_METAC AROK06 methanosarc  
42 43.5 31.3 426 1 DGT1\_PENCH Q8nnh1 corynebacte  
43 43.5 31.3 612 1 PLB1\_PENCH P39457 penicillium  
44 43 30.9 354 1 WN9A\_CHICK O42280 gallus gall  
45 43 30.9 365 1 WN9A\_HUMAN O14904 homo sapien

DR PIR; B32393; B32393.  
 DR DB; 100J; 26-SEP-01.  
 DR MGD; MGI:1101059; Thfrs9.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 1.  
 DR SMART; SM00208; TNFR; 2.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_2; FALSE NEG.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; 3D-structure.  
 FT SIGNAL 1 24  
 FT CHAIN 25 256  
 FT DOMAIN 25 187  
 FT TRANSMEM 188 208  
 FT DOMAIN 209 256  
 FT REPEAT 17 45  
 FT REPEAT 46 85  
 FT REPEAT 86 117  
 FT REPEAT 118 159  
 FT DISULFID 28 37  
 FT DISULFID 31 44  
 FT DISULFID 47 61  
 FT DISULFID 64 77  
 FT DISULFID 67 85  
 FT DISULFID 87 93  
 FT DISULFID 98 105  
 FT DISULFID 101 116  
 FT DISULFID 119 133  
 FT DISULFID 139 158  
 FT CARBOHYD 138 138  
 FT CARBOHYD 138 138  
 SQ SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;  
 Query Match 100.0%; Score 139; DB 1; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-14;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
 DB 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157  
 RESULT 2  
 TN9 HUMAN STANDARD; PRT; 255 AA.  
 AC Q07011;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB ligand receptor) (T-cell antigen 4-1BB homolog) (T-cell antigen ILA) (CD137 antigen).  
 DE (CD137 antigen).  
 GN TNFRSF9 OR ILA OR CD137.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=94374434; PubMed=8088337;  
 RA Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J., Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;  
 RT "Molecular and biological characterization of human 4-1BB and its ligand.";  
 RT Eur. J. Immunol. 24:2219-2227(1994).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=94085794; PubMed=8262389;  
 RA Schwarz H., Tuckwell J., Lotz M.;  
 RT "A receptor induced by lymphocyte activation (ILA): a new member of the human nerve-growth-factor/tumor-necrosis-factor receptor

RT family.";  
 RL Gene 134:295-298(1993).  
 RN [3]  
 RP REVISION TO 107.  
 RA Schwarz H.;  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=95347766; PubMed=7622190;  
 RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E., Kwon B.S.;  
 RL "Characterization of human homologue of 4-1BB and its ligand.";  
 RL Immunol. Lett. 45:67-73(1995).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=95347766; PubMed=7622190;  
 RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E., Kwon B.S.;  
 RL "Characterization of human homologue of 4-1BB and its ligand.";  
 RL Immunol. Lett. 45:67-73(1995).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Hales S., Garcia A.M., Gay L.J., Hultk S.W., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [7]  
 RP INTERACTION WITH TRAF1, TRAF2 AND TRAF3.  
 RX MEDLINE=98078711; PubMed=9418902;  
 RA Arch R.H., Thompson C.B.;  
 RT "4-1BB and OX40 are members of a tumor necrosis factor (TNF)-nerve growth factor receptor subfamily that bind TNF receptor-associated factors and activate nuclear factor kappaB.";  
 RT Mol. Cell. Biol. 18:558-565(1998).  
 RN [8]  
 RP INTERACTION WITH TRAF1 AND TRAF2.  
 RX MEDLINE=98270914; PubMed=9607925;  
 RA Scoulli K., Lee S.Y., Cammons J.L., Yeh W.C., Santana A., Goldstein M.D., Bangia N., DeBenedetto M.A., Mak T.W., Choi Y., Watts T.H.;  
 RT "CD28-independent, TRAF2-dependent costimulation of resting T cells by 4-1BB ligand.";  
 RL J. Exp. Med. 187:1849-1862(1998).  
 RN [9]  
 RP INTERACTION WITH LRR-REPEAT PROTEIN 1/LRR-1.  
 RX MEDLINE=21662677; PubMed=11804328;  
 RA Jiang I.-K., Lee Z.-H., Kim H.-H., Hill J.M., Kim J.-D., Kwon B.S.;  
 RT "A novel leucine-rich repeat protein (LRR-1): potential involvement in 4-1BB-mediated signal transduction.";  
 RL Mol. Cells 12:304-312(2001).  
 CC -|- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T cell activation.  
 CC -|- SUBUNIT: Interacts with TRAF1, TRAF2 AND TRAF3. Interacts with LRR-repeat protein 1/LRR-1.  
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -|- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.  
 CC -|- SIMILARITY: Contains 4 TNFR-Cys repeats.

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CC -!- DATABASE: NAME=PROW; NOTE=CD guide CDW137 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw137.htm".  
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CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL; U03397; AAA5133.1; --  
CC EMBL; L12964; AAA62478.2; --  
CC EMBL; AL009183; CAB57398.1; --  
CC EMBL; BC006196; AAH06196.1; --  
CC PIR; I38426; I38426.  
CC Genew; HGNC:11924; TNFRSF9.  
CC MIM; 602250; --  
CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
CC GO; GO:0004872; F:receptor activity; TAS.  
CC GO; GO:0006317; P:induction of apoptosis; TAS.  
CC GO; GO:0008285; P:negative regulation of cell proliferation; TAS.  
CC InterPro; IPR001369; TNFR_c6.  
CC Pfam; PF00020; TNFR_c6; 2.  
CC SMART; SM00208; TNFR; 2.  
CC PROSITE; PS00652; TNFR_NGFR_1; 1.  
CC PROSITE; PS00650; TNFR_NGFR_2; 1.  
CC Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
KW SIGNAL 1 17 POTENTIAL.  
FT CHAIN 18 255  
FT DOMAIN 18 186  
FT TRANSNEM 187 213  
FT DOMAIN 214 255  
FT REPEAT 17 45  
FT REPEAT 47 86  
FT REPEAT 87 118  
FT REPEAT 119 159  
FT DOMAIN 214 255  
FT DISULFID 28 37  
FT DISULFID 31 45  
FT DISULFID 48 62  
FT DISULFID 65 78  
FT DISULFID 86 94  
FT DISULFID 99 106  
FT DISULFID 102 117  
FT DISULFID 121 133  
FT DISULFID 139 159  
FT CARBOHYD 138 138  
FT CARBOHYD 149 149  
SQ SEQUENCE 255 AA; 27899 MW; F3A563P5EF00460 CRC64;  
  
Query Match 82.78; Score 115; DB 1; Length 255;  
Best Local Similarity 80.0%; Pred. No. 3.2e-10;  
Matches 20; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
Oy 1 CRPWNCSLDGRSVLKTGTTEKDVV 25  
Db 133 CRPWNCSLDGKSVLVNGTKERDVV 157  
  
RESULT 3  
TR11_MOUSE ID Tr11_MOUSE STANDARD; PRT; 625 AA.  
AC O35305; Q8VC7; PRT;  
DT 16-OCT-2001 (Rel. 40, Created)  
DE 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 11A precursor  
DE (Receptor activator of NF-kB) (Osteoclast differentiation factor  
DE receptor) (ODFR).  
GN TNFRSF11A OR RANK.
```

DR Pfam; PF00020; TNFR\_c6; 3.  
 DR SMART; SM00208; TNFR; 4.  
 DR PROSITE; PS00852; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00500; TNFR\_NGFR\_2; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 625  
 FT  
 FT DOMAIN 31 214  
 FT TRANSMEM 215 234  
 FT DOMAIN 235 625  
 FT REPEAT 35 69  
 FT REPEAT 72 113  
 FT REPEAT 115 152  
 FT REPEAT 155 195  
 FT DISULFID 35 47  
 FT DISULFID 48 61  
 FT DISULFID 51 69  
 FT DISULFID 72 87  
 FT DISULFID 93 113  
 FT DISULFID 115 128  
 FT DISULFID 134 152  
 FT CARBOHYD 106 106  
 FT CARBOHYD 175 175  
 FT CONFLICT 494 494  
 SQ SEQUENCE 625 AA; 66621 MW; F8C1872E99511D8E CRC64;  
 Query Match 61.9%; Score 86; DB 1; Length 625;  
 Best Local Similarity 60.0%; Pred. No. 2.4e-05;  
 Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 CRPWTNCSLDGRSVLKTGTEKDVV 25  
 Db 170 CRPWTNCTLLGKLEAHQGTESDVV 194  
 RESULT 4  
 ID TRIL HUMAN STANDARD; PRT; 616 AA.  
 AC Q9YQ6;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 11A precursor  
 DE (Receptor activator of NF-KB) (Osteoclast differentiation factor  
 DE receptor) (ODFR).  
 GN TNFRSF11A OR RANK.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Dendritic cell;  
 RX MEDLINE=98032977; PubMed=9367155;  
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,  
 RA Tonetsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,  
 RA Galibert L.;  
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth  
 RT and dendritic-cell function.";  
 RL Nature 390:175-179(1997).  
 RN [2]  
 RP FUNCTION.  
 RX MEDLINE=98097247; PubMed=9878548;  
 RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,  
 RA Morinaga T., Higashio K.;  
 RT "RANK is the essential signaling receptor for osteoclast  
 RT differentiation factor in osteoclastogenesis.";  
 RL Biochem. Biophys. Res. Commun. 253:395-400(1998).  
 RN [3]  
 RP INTERACTION WITH TRAF1; TRAF2; TRAF3; TRAF5 AND TRAF6.  
 RX MEDLINE=98447691; PubMed=9774460;  
 RA Wong B.R., Josien R., Lee S.Y., Vologodskaya M., Steinman R.M.,  
 RA Choi Y.;  
 RT "The TRAF family of signal transducers mediates NF-kappaB activation  
 RT by the TRANCE receptor.";  
 RL J. Biol. Chem. 273:28355-28359(1998).  
 RN [4]  
 RP VARIANT PEO LEU-LEU-CYS-ALA-LEU-LEU-21 INS, VARIANT PDB2  
 RP ALA-LEU-LEU-LEU-CYS-ALA-LEU-LEU-21 INS, AND VARIANT VAL-192.  
 RX MEDLINE=20082806; PubMed=18615125;  
 RA Hughes A.E., Ralston S.H., Marken J., Bell C., MacPherson H.,  
 RA Wallace R.G.H., van Hul W., Whyte M.P., Nakatsuka K., Hovy L.,  
 RA Anderson D.M.;  
 RT "Mutations in TNFRSF11A, affecting the signal peptide of RANK, cause  
 RT familial expansile osteolysis.";  
 RL Nat. Genet. 24:45-48(2000).  
 CC -!- FUNCTION: Receptor for TNFSF11/RANKL/TRANCE/OPGL; essential for  
 CC RANKL-mediated osteoclastogenesis. Involved in the regulation of  
 CC interactions between T-cells and dendritic cells.  
 CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (potential).  
 CC -!- TISSUE SPECIFICITY: Ubiquitous expression with high levels in  
 CC skeletal muscle, thymus, liver, colon, small intestine and adrenal  
 CC gland.  
 CC -!- DISEASE: Defects in TNFRSF11A are the cause of familial expansile  
 CC osteolysis (FEO) [MIM:174810]. FEO is a rare autosomal dominant  
 CC bone disorder characterized by focal areas of increased bone  
 CC remodelling. The osteolytic lesions develop usually in the long  
 CC bones during early adulthood. FEO is often associated with early  
 CC onset deafness and loss of dentition.  
 CC -!- DISEASE: Defects in TNFRSF11A are a cause of Paget disease of bone  
 CC 2 (PDB2) [MIM:602080]; also known as familial Paget disease of  
 CC bone. PDB2 is a bone remodelling disorder with clinical  
 CC similarities to FEO. Unlike FEO, however, affected individuals  
 CC have involvement of the axial skeleton with lesions in the spine,  
 CC pelvis and skull.  
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC  
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 CC  
 CC EMBL; AF018253; RAB96809.1; -.  
 CC HSSP; P25942; 1CDF.  
 CC Genew; HGNC:11908; TNFRSF11A.  
 CC MIM; 603499; -.  
 CC MIM; 174810; -.  
 CC MIM; 602080; -.  
 CC GO; GO:0004872; F:receptor activity; TAS.  
 CC GO; GO:0007267; P:cell-cell signaling; TAS.  
 CC GO; GO:0008284; P:positive regulation of cell proliferation; TAS.  
 CC GO; GO:0007165; P:signal transduction; TAS.  
 CC InterPro; IPR001368; TNFR\_c6.  
 CC Pfam; PF00020; TNFR\_c6; 4.  
 CC SMART; SM00208; TNFR; 4.  
 CC PROSITE; PS00852; TNFR\_NGFR\_1; 1.  
 CC PROSITE; PS00500; TNFR\_NGFR\_2; 1.  
 CC Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;  
 CC Disease mutation; Deafness.  
 FT SIGNAL 1 29  
 FT CHAIN 30 616  
 FT  
 FT DOMAIN 30 212  
 FT TRANSMEM 213 233  
 FT DOMAIN 234 616  
 FT REPEAT 34 68  
 FT REPEAT 71 112  
 FT REPEAT 114 151  
 FT REPEAT 154 194  
 FT DISULFID 34 46  
 FT DISULFID 47 60



FT DISULFID 50 68 BY SIMILARITY.  
FT DISULFID 71 86 BY SIMILARITY.  
FT DISULFID 92 112 BY SIMILARITY.  
FT DISULFID 114 127 BY SIMILARITY.  
FT DISULFID 133 151 BY SIMILARITY.  
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARIANT 21 21 L -> LALLLCLL (in PDB2).  
FT VARIANT 21 21 L -> LLLCLL (in PBO).  
FT VARIANT 192 192 /FTID=VAR\_011517.  
FT VARIANT 192 192 /FTID=VAR\_011518.  
FT SEQUENCE 616 AA; 66033 MW; E3D9A7A08196F81 CRC64;  
Query Match 54.0%; Score 75; DB 1; Length 616;  
Best Local Similarity 52.0%; Pred. No. 0.0012;  
Matches 13; Conservative 3; Mismatches 9; Indels 0; Gaps 0;  
Qy 1 CRPWTNCSLDGRSVLKTGTEKDVV 25  
Db 169 CRPWTNCTFLGKRVHGHGTEKSDAV 193  
RESULT 5  
TNR4\_HUMAN STANDARD; PRT; 277 AA.  
AC P43489; Q13663;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L  
DE receptor) (ACT35 antigen) (TNF-transcriptionally activated  
DE Glycoprotein 1 receptor) (CD134 antigen).  
GN TNFRSF4 OR TNFR1L.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94170844; PubMed=7510240;  
RA Latza U., Duerkop H., Schnittger S., Ringeling J., Bitelbach F.,  
RA Hummel M., Fonatsch C., Stein H.;  
RT "The human OX40 homolog: cDNA structure, expression and chromosomal  
RT assignment of the ACT35 antigen."  
RL Eur. J. Immunol. 24:677-683(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95219871; PubMed=7704935;  
RA Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,  
RA Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.;  
RT "Identification of OX40 ligand and preliminary characterization of  
RT its activities on OX40 receptor."  
RL Circ. Shock 44:30-34(1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20318724; PubMed=10861060;  
RA Pankow R., Duerkop H., Latza U., Krause H., Kunzendorf U., Pohl T.,  
RA Bulfone-Paus S.;  
RT "The HTLV-I protein transcriptionally modulates OX40 antigen  
RT expression."  
RL J. Immunol. 165:263-270(2000).  
RN [4]  
RP INTERACTION WITH TRAF1; TRAF2 AND TRAF3.  
RX MEDLINE=98078711; PubMed=9418902;  
RA Arch R.H., Thompson C.B.;  
RT "4-1BB and OX40 are members of a tumor necrosis factor (TNF) nerve  
RT growth factor receptor subfamily that bind TNF receptor-associated  
RT factors and activate nuclear kappaB."  
RL Mol. Cell. Biol. 18:558-565(1998).  
RN [5]  
RP INTERACTION WITH TRAF2 AND TRAF5.

RX MEDLINE=98157982; PubMed=9488716;  
RA Kawamata S., Hori T., Imura A., Takaori-Kondo A., Uchiyama T.;  
RT "Activation of OX40 signal transduction pathways leads to tumor  
RT necrosis factor receptor-associated factor (TRAF) 2- and  
RT TRAF5-mediated NF-kappaB activation."  
RL J. Biol. Chem. 273:5808-5814(1998).  
CC - FUNCTION: Receptor for TNFSF4/OX40L/SP34.  
CC - SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5.  
CC - SUBCELLULAR LOCATION: Type I membrane protein.  
CC - SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC - DATABASE: NAME=PROW; NOTE=CD guide CD134 entry; htm".  
WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd134.htm".  
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CC  
CC EMBL; X75962; CAA53576.1; -  
DR EMBL; S76792; AAB33944.1; ALT INIT.  
DR EMBL; AJ27151; CAB96543.1; -  
DR PIR; I37552; I37552.  
DR HSP; OL4763; IDOG.  
DR Genew; HGNC:11918; TNFRSF4.  
DR MIM; 600315; -  
DR GO; GO:0005887; C: integral to plasma membrane; TAS.  
DR GO; GO:0005027; F: NGF/TNF (6 C-domain) receptor activity; TAS.  
DR GO; GO:0006955; P: immune response; TAS.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE; PS00500; TNFR\_NGFR\_2; 2.  
KW Receptor; Antigen; Transmembrane; Glycoprotein; Repeat; Signal.  
FT SIGNAL 28 POTENTIAL.  
FT CHAIN 29 277 TUMOR NECROSIS FACTOR RECEPTOR  
FT  
FT DOMAIN 29 214 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 215 235 POTENTIAL.  
FT DOMAIN 236 277 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 30 65 TNFR-CYS 1.  
FT REPEAT 66 107 TNFR-CYS 2. (INCOMPLETE).  
FT REPEAT 108 126 TNFR-CYS 3. (INCOMPLETE).  
FT REPEAT 127 167 TNFR-CYS 4.  
FT DISULFID 31 42 BY SIMILARITY.  
FT DISULFID 43 56 BY SIMILARITY.  
FT DISULFID 46 64 BY SIMILARITY.  
FT DISULFID 67 81 BY SIMILARITY.  
FT DISULFID 84 99 BY SIMILARITY.  
FT DISULFID 87 107 BY SIMILARITY.  
FT DISULFID 109 125 BY SIMILARITY.  
FT DISULFID 128 141 BY SIMILARITY.  
FT DISULFID 147 166 BY SIMILARITY.  
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 277 AA; 29340 MW; 49F15525941550BF CRC64;  
Query Match 52.5%; Score 73; DB 1; Length 277;  
Best Local Similarity 40.0%; Pred. No. 0.00097;  
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;  
Qy 1 CRPWTNCSLDGRSVLKTGTEKDVV 25  
Db 141 CRPWTNCTLAGKHTLQPASNSDAI 165  
RESULT 6  
TNR4\_RAT  
ID TNR4\_RAT STANDARD; PRT; 271 AA.  
AC P15725;

DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L  
 GN TNFRSF4 OR TXGPF1L OR OX40.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=90214614; PubMed=2157591;  
 RX Mallett S., Fossum S., Barclay A.N.;  
 RA "Characterization of the MRC OX40 antigen of activated CD4 positive T  
 RL lymphocytes -- a molecule related to nerve growth factor receptor.";  
 EMBO J. 9:1063-1068(1990).  
 CC -!- FUNCTION: Receptor for TNFRSF4/OX40L/GP34.  
 CC -!- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- TISSUE SPECIFICITY: ACTIVATED T-CELLS.  
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
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 CC  
 DR EMBL; X17037; CAA34897.1; -  
 DR PIR; S12783; S12783.  
 DR HSSP; O14763; 1D4V.  
 DR InterPro; IPR001368; TNFR\_C6.  
 DR Pfam; PF00020; TNFR\_C6; 3.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS00500; TNFR\_NGFR\_2; 2.  
 KW Receptor; Antigen; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 271  
 FT DOMAIN 20 210  
 FT TRANSMEM 211 235  
 FT REPEAT 25 60  
 FT REPEAT 61 102  
 FT REPEAT 103 123  
 FT REPEAT 124 164  
 FT DISULFID 26 37  
 FT DISULFID 38 51  
 FT DISULFID 41 59  
 FT DISULFID 62 76  
 FT DISULFID 79 94  
 FT DISULFID 82 102  
 FT DISULFID 104 122  
 FT DISULFID 125 138  
 FT DISULFID 144 163  
 FT CARBOHYD 143 143  
 SQ SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;  
 Query Match 50.4%; Score 70; DB 1; Length 271;  
 Best Local Similarity 40.0%; Pred. No. 0.0027;  
 Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 CRPWTNCSLDGRSVLTKTTTQDVV 25  
 DB 138 CKPWTNCTLSGQIRHPASNSLDTV 162  
 RESULT 7

TNR4 MOUSE  
 ID TNR4 MOUSE STANDARD; PRT; 272 AA.  
 AC P47741;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L  
 GN TNFRSF4 OR TXGPF1L OR OX40.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=94044750; PubMed=8228223;  
 RA Calderhead D.M., Buhmann J.E., van den Bertwegh A.J.,  
 RA Claassen E., Noelle R.J., Fell H.;  
 RT "Cloning of mouse OX40: a T cell activation marker that may mediate  
 RT T-B cell interactions."; J. Immunol. 151:5261-5271(1993).  
 RL J. Immunol. 151:5261-5271(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95255413; PubMed=7737295;  
 RA Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,  
 RA Barclay A.N.;  
 RT "Gene structure and chromosomal localization of the mouse homologue  
 RT of rat OX40 protein."; Eur. J. Immunol. 25:926-930(1995).  
 RL Eur. J. Immunol. 25:926-930(1995).  
 CC -!- FUNCTION: Receptor for TNFRSF4/OX40L/GP34.  
 CC -!- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
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 CC  
 DR EMBL; Z21674; CAA79772.1; -  
 DR EMBL; X85214; CAA59476.1; -  
 DR PIR; I48700; I48700.  
 DR HSSP; O14763; 1D0G.  
 DR MGD; MG1:104512; Tnfrsf4.  
 DR GO; GO:0005886; C:plasma membrane; IDA.  
 DR GO; GO:0006968; P:cellular defense response; IMP.  
 DR InterPro; IPR001368; TNFR\_C6.  
 DR Pfam; PF00020; TNFR\_C6; 3.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS00500; TNFR\_NGFR\_2; 2.  
 KW Receptor; Antigen; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 272  
 FT DOMAIN 20 211  
 FT TRANSMEM 212 236  
 FT REPEAT 26 61  
 FT REPEAT 62 103  
 FT REPEAT 104 124  
 FT REPEAT 125 165  
 FT DISULFID 27 38  
 FT DISULFID 39 52  
 FT DISULFID 42 60  
 FT DISULFID 63 77  
 FT DISULFID 80 95  
 FT DISULFID 83 103  
 FT DISULFID 105 123

[4] SEQUENCE FROM N.A. (ISOFORM I).  
 TISSUE:Ovary;  
 MEDLINE=22388257; PubMed=12477932;  
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettelman M., Maman A., Rodrigues S., Sanchez A.,  
 Whitting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [5] INTERACTION WITH TRAF3.  
 MEDLINE=95184010; PubMed=7533327;  
 Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;  
 "Involvement of CRAF1, a relative of TRAF, in CD40 signaling.";  
 Science 287:1494-1498(1995).  
 [6] INTERACTION WITH TRAF3.  
 MEDLINE=95129692; PubMed=7530216;  
 Sato T., Irie S., Reed J.C.;  
 "A novel member of the TRAF family of putative signal transducing  
 proteins binds to the cytosolic domain of CD40.";  
 FEBS Lett. 358:113-118(1995).  
 [7] INTERACTION WITH TRAF1, TRAF2, TRAF3 AND TRAF5.  
 MEDLINE=98384149; PubMed=9718306;  
 Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J.,  
 Kehry M.R.;  
 "CD40-tumor necrosis factor receptor-associated factor (TRAF)  
 interactions: regulation of CD40 signaling through multiple TRAF  
 binding sites and TRAF hetero-oligomerization.";  
 Biochemistry 37:11836-11845(1998).  
 [8] INTERACTION WITH TRAF5.  
 MEDLINE=98172745; PubMed=9511754;  
 Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,  
 Otsuka M., Yamamoto I., Inoue J.-I.;  
 "Cloning and characterization of a cDNA encoding the human homolog of  
 tumor necrosis factor receptor-associated factor 5 (TRAF5).";  
 Gene 207:135-140(1998).  
 [9] INTERACTION WITH TRAF6.  
 MEDLINE=98095703; PubMed=9432981;  
 Kashiwada M., Shirakata Y., Inoue J.-I., Nakano H., Okazaki K.,  
 Okumura K., Yamamoto T., Nagasaka H., Takemori T.;  
 "Tumor necrosis factor receptor-associated factor 6 (TRAF6) stimulates  
 extracellular signal-regulated kinase (ERK) activity in CD40  
 signaling along a ras-independent pathway";  
 J. Exp. Med. 187:237-244(1998).  
 [10] 3D-STRUCTURE MODELING OF 24-144.  
 MEDLINE=97189482; PubMed=9037712;  
 Bajorath J., Aruffo A.;  
 "Construction and analysis of a detailed three-dimensional model of  
 the ligand binding domain of the human B cell receptor CD40.";  
 Proteins 27:59-70(1997).  
 [11] 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.  
 MEDLINE=98266353; PubMed=9605317;

RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,  
 RA Zheng Z., Naismith J.H., Thomas D.;  
 RT "The role of polar interactions in the molecular recognition of CD40L  
 RT with its receptor CD40.";  
 RL Protein Sci. 7:1124-1135(1998).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 247-266 IN COMPLEX WITH  
 RP TRAF3.  
 RX MEDLINE=20442386; PubMed=10984535;  
 RA Ni C.Z., Welsh K., Leo E., Chiu C.K., Wu H., Reed J.C., Ely K.R.;  
 RT "Molecular basis for CD40 signaling mediated by TRAF3.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:10395-10399(2000).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 178-195 IN COMPLEX WITH  
 RP TRAF3.  
 RX MEDLINE=22000222; PubMed=12005438;  
 RA Li C., Ni C.Z., Havert M.L., Cabezas E., He J., Kaiser D., Reed J.C.,  
 RA Satterthwait A.C., Cheng G., Ely K.R.;  
 RT "Downstream regulator TRAF3 binds to the CD40 recognition site on  
 RT TRAF3.";  
 RL Structure 10:403-411(2002).  
 RN [14]  
 RP VARIANT HIGM3 ARG-83.  
 RX MEDLINE=21532985; PubMed=11675497;  
 RA Ferrari S., Gilliani S., Inesalco A., Al-Chonaim A., Soresina A.R.,  
 RA Loubser M., Avanzini M.A., Marconi M., Badolatto R., Ugazio A.G.,  
 RA Levy Y., Catalan N., Durandy A., Thakni A., Notarangelo L.D.,  
 RA Plebani A.;  
 RT "Mutations of CD40 gene cause an autosomal recessive form of  
 RT immunodeficiency with hyper IgM.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12614-12619(2001).  
 CC -!- FUNCTION: Receptor for TNFRSF5/CD40L.  
 CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform I);  
 CC secreted (isoform II).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=I;  
 CC IsoId=P25942-1; Sequence=Displayed;  
 CC Name=II;  
 CC IsoId=P25942-2; Sequence=VSP 006472, VSP 006473;  
 CC -!- TISSUE SPECIFICITY: B-cells and in primary carcinomas.  
 CC -!- DISEASE: Defects in TNFRSF5 are the cause of hyper-IgM  
 CC immunodeficiency type 3 (HIGM3) [MIM:606843]. HIGM3 is an  
 CC autosomal recessive disorder which includes an inability of B  
 CC cells to undergo isotype switching, one of the final  
 CC differentiation steps in the humoral immune system, and an inability  
 CC to mount an antibody-specific immune response, and a lack of  
 CC germinal center formation.  
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -!- DATABASE: NAME=PRO; NOTE=CD guide CD40 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/protow/cd/cd40.htm".  
 CC -----  
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 CC -----  
 CC EMBL; X60592; CAA43045.1; -  
 CC EMBL; AL035662; CAC17670.1; -  
 CC EMBL; AJ300189; CAC29424.1; -  
 CC EMBL; BC012419; AAH12419.1; -  
 CC PIR; S04460; A60771.  
 CC PDB; 1CDF; 01-APR-97.  
 CC PDB; 1FLF; 18-OCT-00.  
 CC PDB; 1LOA; 08-FEB-00.  
 CC PDB; 1CZ2; 26-SEP-01.  
 CC -----  
 CC Query Match 45.3%; Score 63; DB 1; Length 277;

Best Local Similarity 44.0%; Pred. No. 0.033;  
 Matches 11; Conservative 3; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 CRPWTNCSLDGRSVLTKGTETKDVV 25  
 Db 161 CRPWTNCSLTKLVVQAGTKTDVW 185  
 RESULT 9  
 ID TNRS MOUSE STANDARD; PRT: 289 AA.  
 AC P27512; Q99NE0; Q99NE1; Q99NE2; Q99NE3;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 5 precursor  
 DE (CD40L receptor) (B-cell surface antigen CD40) (BP50) (CDw40).  
 GN TNFRSF5 OR CD40.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM I).  
 RX MEDLINE=92105763; PubMed=1370315;  
 RA Torres R.M., Clark E.A.;  
 RT "Differential increase of an alternatively polyadenylated mRNA  
 RT species of murine CD40 upon B lymphocyte activation.";  
 RL J. Immunol. 148:620-626(1992).  
 RN [2]  
 RP REVISIONS.  
 RC STRAIN=BALB/c;  
 RA Torres R.M.;  
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM I).  
 RC STRAIN=BALB/c; TISSUE=Liver;  
 RX MEDLINE=93094586; PubMed=1281194;  
 RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,  
 RA Howard M., Cockayne D.A.;  
 RT "Genomic structure and chromosomal mapping of the murine CD40 gene.";  
 RL J. Immunol. 149:3921-3926(1992).  
 RN [4]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS II; III; IV AND  
 RP V).  
 RX MEDLINE=21117110; PubMed=11172023;  
 RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;  
 RT "Regulation of CD40 function by its isoforms generated through  
 RT alternative splicing.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).  
 RN [5]  
 RP INTERACTION WITH TRAF3.  
 RX MEDLINE=95184010; PubMed=7533327;  
 RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;  
 RT "Involvement of CRAPI, a relative of TRAF, in CD40 signaling.";  
 RL Science 267:1494-1498(1995).  
 RN [6]  
 RP INTERACTION WITH TRAF5.  
 RX MEDLINE=96382484; PubMed=8790348;  
 RA Ishida T., Tojo T., Aoki T., Kobayashi N., Ohishi T., Watanabe T.,  
 RA Yamamoto T., Inoue J.-I.;  
 RT TRAF5, a novel tumor necrosis factor receptor-associated factor  
 RT family protein, mediates CD40 signaling.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:9437-9442(1996).  
 CC -!- FUNCTION: Receptor for TNFRSF5/CD40L.  
 CC -!- SUBUNIT: Interacts with TRAF3 and TRAF5. Interacts with TRAF1,  
 CC TRAF2 and TRAF6 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms I, III, IV  
 CC and V); secreted (isoform II).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=5;  
 CC Name=I;  
 CC IsoId=P27512-1; Sequence=Displayed;  
 CC

Name=II;	CC
Isoid=p27512-2; Sequence=VSP_006474, VSP_006475;	CC
Name=III;	CC
Isoid=p27512-3; Sequence=VSP_006477, VSP_006478;	CC
Name=IV;	CC
Isoid=p27512-4; Sequence=VSP_006479, VSP_006480;	CC
Name=V;	CC
Isoid=p27512-5; Sequence=VSP_006476;	CC
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.	CC
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EMBL; M83312; AAB08705.1; -	DR
EMBL; N94126; AAA37404.1; -	DR
EMBL; N94129; AAA37404.1; JOINED.	DR
EMBL; N94128; AAA37404.1; JOINED.	DR
EMBL; N94127; AAA37404.1; JOINED.	DR
EMBL; AJ401387; CAC29427.1; -	DR
EMBL; AJ401388; CAC29428.1; -	DR
EMBL; AJ401389; CAC29429.1; -	DR
EMBL; AJ401390; CAC29430.1; -	DR
PIR; A46476; A46476.	DR
HSP; P25942; ICBF.	DR
MGI; 88336; Tnfrsf5.	DR
InterPro; IPRO08063; Fas_receptor.	DR
InterPro; IPRO01368; TNFR_C6.	DR
Pfam; PF00020; TNFR_C6; 4.	DR
PRINTS; PR01680; FASRECEPTOR.	DR
SMART; SM00208; TNFR; 4.	DR
PROSITE; PS00652; TNFR_NGFR_1; 1.	DR
PROSITE; PS00505; TNFR_NGFR_2; 4.	DR
KW Receptor; Transmembrane; glycoprotein; Repeat; Signal;	KW
Alternative splicing.	KW
SIGNAL 1	FT
CHAIN 20 289	FT
TUMOR NECROSIS FACTOR RECEPTOR	FT
SUPERFAMILY MEMBER 5.	FT
EXTRACELLULAR (POTENTIAL).	FT
CYTOTOPLASMIC (POTENTIAL).	FT
TNFR-CYS 1.	FT
TNFR-CYS 2.	FT
TNFR-CYS 3.	FT
TNFR-CYS 4.	FT
BY SIMILARITY.	FT
BY SIMILARITY.	FT
BY SIMILARITY.	FT
BY SIMILARITY.	FT
BY SIMILARITY.	FT
BY SIMILARITY.	FT
N-LINKED (GLCNAC... ) (POTENTIAL).	FT
SCEDKNLEVIQKTSQTNNVICGLSKSRALLVPVMG -->	FT
RFKVPDASPAGHSGCDGHPPHPRGVSLYQKGQETKG	FT
(in isoform II).	FT
/FTid=VSP_006474.	FT
Missing (in isoform II).	FT
/FTid=VSP_006475.	FT
GLKRMRLALVPVMGILLITFGVFLYIK -> E (in isoform V).	FT
/FTid=VSP_006476.	FT
KKVKPKPKDNEMEPFAARR -> SECSGEREGGFSPVEPA	FT
S (in isoform III).	FT
/FTid=VSP_006477.	FT
Missing (in isoform III).	FT
/FTid=VSP_006478.	FT
KKWKPK -> SGOETKG (in isoform IV).	FT

```
RESULT 11
TNF5_BOVIN STANDARD; PRT; 269 AA.
ID Q28203;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (Fragment).
GN TNFRSF5 OR CD40.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97281252; PubMed=9135560;
RA Hirano A., Brown W.C., Estes D.M.;
RT "Cloning, expression and biological function of the bovine CD40
RT homologue: role in B-lymphocyte growth and differentiation in
RT cattle.";
RL Immunology 90:294-300(1997).
CC -!- FUNCTION: Receptor for TNFRSF5/CD40L.
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
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CC -----
DR EMBL; U57745; AAC48710.1; -.
DR HSRP; P25942; 1CDF.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_C6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 1.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 19
FT CHAIN 20 >269
FT DOMAIN 20 193
FT TRANSMEM 194 215
FT DOMAIN 216 >269
FT REPEAT 25 60
FT REPEAT 61 103
FT REPEAT 104 144
FT REPEAT 145 187
FT DISULFID 26 37
FT DISULFID 38 51
FT DISULFID 41 59
FT DISULFID 62 77
FT DISULFID 83 103
FT DISULFID 105 119
FT DISULFID 111 116
FT DISULFID 125 143
FT CARBOHYD 153 153
FT CARBOHYD 180 180
FT NON_TER 269
SQ SEQUENCE 269 AA; 29983 MW; 746903F30F95F387 CRC64;
Query Match 37.4%; Score 52; DB 1; Length 269;
Best Local Similarity 40.0%; Pred. No. 1.5;
Matches 10; Conservative 2; Mismatches 13; Indels 0; Gaps 0;
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Oy 1 CRPTWNCSLDGRSVLKTGTEKDVV 25
Db 161 CHERWTCERKGLVEHQVGNKTDV 185

RESULT 12
TR21_HUMAN STANDARD; PRT; 555 AA.
ID TR21_HUMAN STANDARD; PRT; 555 AA.
AC O75509; Q96D86;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-
DE related death receptor-6) (Death receptor 6).
GN TNFRSF21 OR DR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98378343; PubMed=9714541;
RA Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Yu G., Vincenz C.,
RA Aggarwal B.B., Ni J., Dixit V.M.;
RT "Identification and functional characterization of DR6, a novel death
RT domain-containing TNF receptor.";
RL PNAS Lett. 431:351-356(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Parker A.; (FEB-2000) to the EMBL/GenBank/DBJ databases.
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
CC -!- SUBUNIT: Associates with TRADD.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, brain, placenta,
CC pancreas, lymph node, thymus and prostate. Detected at lower
CC levels in lung, skeletal muscle, kidney, testis, uterus, small
CC intestine, colon, spleen, bone marrow and fetal liver. Very low
CC levels were found in adult liver and peripheral blood leukocytes.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-25 is the initiator.
CC -----
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CC EMBL: AF068868; RAC34583.1; -  
 CC EMBL: AL096801; CAB75692.1; -  
 DR EMBL: BC017730; RAH17730.1; -  
 DR EMBL: BC010241; RAH10241.1; ALT\_INIT.  
 DR HSSP: O14763; LD0G.  
 DR Genew; HGNC:13469; TNFRSF21.  
 DR MIM; 605732; -  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00531; death.1.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 1.  
 DR PROSITE; PS0017; DEATH DOMAIN; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 1.  
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 41  
 FT CHAIN 42 655  
 FT DOMAIN 42 349  
 FT TRANSMEM 350 370  
 FT DOMAIN 371 655  
 FT DOMAIN 415 498  
 FT REPEAT 50 88  
 FT REPEAT 90 131  
 FT REPEAT 133 167  
 FT REPEAT 170 211  
 FT REPEAT 67 80  
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 FT DISULFID 91 106  
 FT DISULFID 109 123  
 FT DISULFID 131 131  
 FT DISULFID 133 144  
 FT DISULFID 150 168  
 FT DISULFID 171 186  
 FT DISULFID 192 211  
 FT CARBOHYD 82 82  
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 FT CARBOHYD 252 252  
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 FT CARBOHYD 278 278  
 FT CARBOHYD 289 289  
 SQ SEQUENCE 655 AA; 71844 MW; 48939391C4852A33 CRC64;

Query Match 36.0%; Score 50; DB 1; Length 655;  
 Best Local Similarity 40.0%; Pred. No. 8.4;  
 Matches 10; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
 Db 186 KAYTDCLSQNLVVKETGTEDV 210

-----

RESULT 13  
 TRLT\_MACFA  
 ID \_TLT\_MACFA STANDARD; PRT; 430 AA.  
 AC QN092;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 19L precursor  
 DE (Receptor expressed in lymphoid tissues).  
 GN TNFRSF19L OR TRLT.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OC NCBI\_TaxID=9541;  
 RN [1]

SEQUENCE FROM N.A.  
 RP TISSUE=Brain;  
 RC MEDLINE=1459551; PubMed=11574149;  
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirata M., Suto Y.,  
 RA Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K., Kusuda J.,  
 RT "Assignment of 118 novel cDNAs of cynomolgus monkey brain to human  
 chromosomes.";  
 RL Gene 275:31-37(2001).  
 CC -!- FUNCTION: Mediates activation of NF-kappa-B (By similarity). May  
 CC play a role in T-cell activation.  
 CC -!- SUBUNIT: Associates with TRAF1 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
 CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.  
 CC -----  
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CC EMBL: AB046039; BAB01621.1; -  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR SMART; SM00208; TNFR; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; FALSE NEG.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; FALSE NEG.  
 KW Receptor; Transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 1 26  
 FT CHAIN 27 430  
 FT DOMAIN 27 162  
 FT TRANSMEM 163 183  
 FT DOMAIN 184 430  
 FT REPEAT 50 90  
 FT REPEAT 51 65  
 FT DISULFID 71 90  
 FT DISULFID 149 149  
 FT CARBOHYD 149 149  
 SQ SEQUENCE 430 AA; 45850 MW; BA8DE92593E1E859 CRC64;

Query Match 35.3%; Score 49; DB 1; Length 430;  
 Best Local Similarity 36.0%; Pred. No. 7.5;  
 Matches 9; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
 Db 65 CQPWARCQLRRLEAQVGTATDIL 89

-----

RESULT 14  
 YEW6\_YEAST  
 ID YEW6\_YEAST STANDARD; PRT; 175 AA.  
 AC P38268;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Very hypothetical 20.2 kDa protein in LYS2-TKL2 intergenic region.  
 GN YER116C OR YER0911.  
 OS Saccharomyces cerevisiae (baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OC NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288c;  
 RX MEDLINE=95208357; PubMed=7900426;  
 RA Mannhaupt G., Stucka R., Ehrlie S., Vetter I., Feldmann H.;  
 RT "Analysis of a 70 kb region on the right arm of yeast chromosome II.";  
 RL Yeast 10:1363-1381(1994).  
 CC -----  
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DR ENBL; X78993; CAA55618.1; -  
DR EMBL; Z35985; CAA85073.1; -  
DR PIR; S48280; S48280.  
DR GERMOnline; 138659; -  
DR SGD; S0000320; YBR116C.  
KW Hypochemical protein; Transmembrane.  
FT TRANSMEM 143 166 POTENTIAL.  
SQ SEQUENCE 175 AA; 20215 MW; 6CF72CC0909E055E CRC64;

Query Match 34.5%; Score 48; DB 1; Length 175;  
Best Local Similarity 38.1%; Pred No. 3.9;  
Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 4 WTNCSDGSRVLKGTTEKDV 24  
Db 76 FTNCISQRTVLRLQGLKQSI 96

## RESULT 15

CSR3\_HUMAN  
ID CSR3\_HUMAN STANDARD; PRT; 194 AA.  
AC P50461; Q9P131;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE LIM domain protein, cardiac (Muscle LIM protein) (Cysteine-rich  
DE protein 3) (CRP3).  
GN CSR3 OR CLP OR MLP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_TaxID=9606;  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RX MEDLINE=96039282; PubMed=7490106;  
RA Fung Y.W., Wang R.X., Heng H.H.Q., Liew C.C.;  
RT "Mapping of a human LIM protein (CLP) to human chromosome 11p15.1 by  
RT fluorescence in situ hybridization.";  
RL Genomics 28:602-603(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Muscle;  
RA Medvedev A., Jettan A.M.;  
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Yasunaga S., Harada H., Kimura A.;  
RT "Cloning and characterization of the human muscle LIM protein gene.";  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart, and Skeletal muscle;  
RA Chen K.H., Zhang J.F., Ma D.L., Tang J.;  
RT "A novel member of LIM gene family involved in cardiovascular  
RT diseases.";  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skeletal muscle, and Testis;  
RX MEDLINE=22389257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [6]  
RP VARIANT CMDIM ARG-4.  
RX MEDLINE=22395799; PubMed=12507422;  
RA Kneill R., Hoshijima M., Hoffman H.M., Person V., Lorenzen-Schmidt I.,  
RA Bang M.-L., Hayashi T., Shiga N., Yasukawa H., Schaper W., McKenna W.,  
RA Yokoyama M., Schork N.J., Omens J.H., McCulloch A.D., Kimura A.,  
RA Gregorio C.C., Poller W., Schaper J., Schultheiss H.P., Chien K.R.;  
RT "The cardiac mechanical stretch sensor machinery involves a Z disc  
RT complex that is defective in a subset of human dilated  
RT cardiomyopathy.";  
RL Cell 111:943-955(2002).  
CC -I- FUNCTION: Positive regulator of myogenesis. Could play a role in  
CC mechanical stretch sensing.  
CC -I- SUBCELLULAR LOCATION: Nuclear, associates with the actin  
CC cytoskeleton (Potential).  
CC -I- TISSUE SPECIFICITY: Cardiac and slow-twitch skeletal muscles.  
CC -I- DISEASE: Defects in CSR3 are the cause of dilated cardiomyopathy  
CC IM (CMDIM) [MIM:607482], a disorder characterized by cardiac  
CC dilation and reduced systolic function.  
CC -I- SIMILARITY: Contains 2 LIM zinc-binding domains.  
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CC EMBL; U20324; AAA91104.1; -  
DR EMBL; U49837; AAA92571.1; -  
DR EMBL; U72898; AAD00189.1; -  
DR EMBL; U72894; AAD00189.1; JOINED.  
DR EMBL; U72895; AAD00189.1; JOINED.  
DR EMBL; U72896; AAD00189.1; JOINED.  
DR EMBL; U72897; AAD00189.1; JOINED.  
DR EMBL; U72899; AAD00183.1; -  
DR EMBL; AF121260; AAF28868.1; -  
DR EMBL; BC005900; AAH05900.1; -  
DR EMBL; BC024010; AAH24010.1; -  
DR EMBL; BC057221; AAH57221.1; -  
DR HSSP; Q05158; 1QLI.  
DR Genew; HGNC:2472; CSR3.  
DR MIM; 600824; -  
DR MIM; 607482; -  
DR GO; GO:0007519; P:myogenesis; TAS.  
DR InterPro; IPR001781; LIM.  
DR Pfam; PF00412; LIM; 2.  
DR ProDom; PD000094; LIM; 2.  
DR SMART; SM00132; LIM; 2.  
DR PROSITE; PS00478; LIM\_DOMAIN\_1; 2.  
DR PROSITE; PS00023; LIM\_DOMAIN\_2; 2.  
KW Nuclear protein; Repeat; LIM domain; Metal-binding; Zinc; Myogenesis;  
Disease mutation.  
FT DOMAIN 10 61 LIM 1.  
FT DOMAIN 63 78 GLY-RICH.  
FT DOMAIN 64 69 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT DOMAIN 120 171 LIM 2.  
FT DOMAIN 177 185 GLY-RICH.  
FT VARIANT 4 W -> R (in CMDIM).



FT FT CONFLICT 26 /FTID=VAR 015401.  
FT SEQUENCE 194 AA; 20969 MW; FDB6E4F8D258C35F CRC64;  
SQ  
Query Match 34.5%; Score 48; DB 1; Length 194;  
Best Local Similarity 34.6%; Pred. No. 4.4;  
Matches 9; Conservative 6; Mismatches 7; Indels 4; Gaps 1;  
QY 2 RPW----TNCSLDGRSVLKTGTTEKD 23  
DB 138 KPWHTCFRCAICGKSLSTNVTDKD 163  
RESULT 16  
CSR3\_MOUSE  
ID CSR3\_MOUSE STANDARD; PRT; 194 AA.  
AC P50462;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE LIM domain protein, cardiac (Muscle LIM protein) (Cysteine-rich  
protein 3) (CRP3).  
DE protein 3) (CRP3).  
GN CSR3 OR CLIP OR MLP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RP STRAIN=MEL1; TISSUE=Mandible;  
RX MEDLINE=9636959; PubMed=8773899;  
RA Harrod G.V., Kettunen P.J., Jowett A.K.;  
RT "Murine MLP: cloning and expression in the embryonic head";  
RL J. Craniofac. Genet. Dev. Biol. 16:65-73(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RP STRAIN=C3H;  
RC Hashimoto N., Ogashiwa M.;  
RA Hattori M., Ogasawara M.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RP TISSUE=Liver;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Brownstein M.J., Soares M.B., Bonaudo M.F., Casavant T.L., Scheetz T.E.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Positive regulator of myogenesis.  
CC -!- SUBCELLULAR LOCATION: Nuclear, associates with the actin  
cytoskeleton (Potential).  
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.  
-----  
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-----  
CC EMBL; X81193; CAA57065.1;  
CC FIR; A55099; A55099.  
CC HSP; Q05158; IQLI.  
CC InterPro; IPR001781; LIM.  
CC Pfam; PF00412; LIM; 2.

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CC or send an email to license@isb-sib.ch).  
-----  
CC EMBL; Z49883; CAA90039.1;  
CC EMBL; D88791; BAA13721.1;  
CC EMBL; BC061131; AAB61131.1;  
CC PIR; S57472; S57472.  
CC HSP; Q05158; IQLI.  
CC MGD; MGI:1330824; Cerp3.  
CC InterPro; IPR001781; LIM.  
CC Pfam; PF00412; LIM; 2.  
CC ProDom; PD000094; LIM; 2.  
CC SMART; SM00132; LIM; 2.  
CC PROSITE; PS00478; LIM DOMAIN 1; 2.  
CC PROSITE; PS00023; LIM DOMAIN 2; 2.  
KW Nuclear protein; Repeat; LIM domain; Metal-binding; Zinc; Myogenesis.  
FT DOMAIN 10 61  
FT DOMAIN 63 78  
FT DOMAIN 64 69  
FT DOMAIN 120 171  
FT DOMAIN 177 185  
FT SEQUENCE 194 AA; 20895 MW; E35CF30CA17CB227 CRC64;  
SQ  
Query Match 34.5%; Score 48; DB 1; Length 194;  
Best Local Similarity 34.6%; Pred. No. 4.4;  
Matches 9; Conservative 6; Mismatches 7; Indels 4; Gaps 1;  
QY 2 RPW----TNCSLDGRSVLKTGTTEKD 23  
DB 138 KPWHTCFRCAICGKSLSTNVTDKD 163  
RESULT 17  
CSR3\_RAT  
ID CSR3\_RAT STANDARD; PRT; 194 AA.  
AC P50463;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE LIM domain protein, cardiac (Muscle LIM protein) (Cysteine-rich  
protein 3) (CRP3).  
DE protein 3) (CRP3).  
GN CSR3 OR CLIP OR MLP.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RP STRAIN=Lewis; TISSUE=Skeletal muscle;  
RX MEDLINE=9504720; PubMed=7954791;  
RA Arber S., Halder G., Caroni P.;  
RT "Muscle LIM protein, a novel essential regulator of myogenesis,  
promotes myogenic differentiation";  
RL Cell 79:221-231(1994).  
CC -!- FUNCTION: Positive regulator of myogenesis.  
CC -!- SUBCELLULAR LOCATION: Nuclear, associates with the actin  
cytoskeleton.  
CC -!- TISSUE SPECIFICITY: High in striated muscle and adult heart.  
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.  
-----  
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-----  
CC EMBL; X81193; CAA57065.1;  
CC FIR; A55099; A55099.  
CC HSP; Q05158; IQLI.  
CC InterPro; IPR001781; LIM.  
CC Pfam; PF00412; LIM; 2.

DR ProDom; PD000094; LIM; 2.  
DR SMART; SM00132; LIM; 2.  
DR PROSITE; PS00478; LIM DOMAIN 1; 2.  
DR PROSITE; PS0023; LIM DOMAIN 2; 2.  
KW Nuclear protein; Repeat; LIM domain; Metal-binding; Zinc; Myogenesis.  
FT DOMAIN 10 61 LIM 1.  
FT DOMAIN 63 78 GLY-RICH.  
FT DOMAIN 64 69 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT DOMAIN 120 171 LIM 2.  
FT DOMAIN 177 185 GLY-RICH.  
SQ SEQUENCE 194 AA; 20803 MW; 2D6848C271BA7EAB CRC64;

Query Match 34.5%; Score 48; DB 1; Length 194;  
Best Local Similarity 34.6%; Pred. No. 4.4;  
Matches 9; Conservative 6; Mismatches 7; Indels 4; Gaps 1;

QY 2 RPTN-----CSLDGRSVLTGTETXD 23

Db 138 KPWHTCFFCAICGKSLSTNVTDKD 163

## RESULT 18

TR18 MOUSE  
ID TE18 MOUSE STANDARD; PRT; 228 AA.  
AC Q35714; Q9UKR1; Q9UKR2; Q9UKR3;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 18 precursor  
DE (Glucocorticoid-induced TNFR-related protein).  
GN TNFRSF18 OR GITR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1] :  
RP SEQUENCE FROM N.A. (ISOFORM A).  
RC STRAIN=C3H;  
RX MEDLINE=97322352; PubMed=9177197;  
RA Nocentini G., Giunchi L., Ronchetti S., Kraus L.T., Bartoli A.,  
Moraca R., Migliorati G., Riccardi C.;  
RT "A new member of the tumor necrosis factor/nerve growth factor  
receptor family inhibits T cell receptor-induced apoptosis.";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM A).  
RC STRAIN=BALE/c;  
RX MEDLINE=20256302; PubMed=10798444;  
RA Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,  
Delfino D., Migliorati G., Riccardi C.;  
RT "Gene structure and chromosomal assignment of mouse GITR, a member of  
the tumor necrosis factor/nerve growth factor receptor family.";  
RL DNA Cell Biol. 19:205-217(2000).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D).  
RC TISSUE=Thymus;  
RX MEDLINE=20292073; PubMed=10836847;  
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,  
Brunetti L., Migliorati G., Riccardi C.;  
RT "Identification of three novel mRNA splice variants of GITR.";  
RL Cell Death Differ. 7:408-410(2000).  
CC -!- FUNCTION: Receptor for TNFSF18. Seems to be involved in  
interactions between activated T lymphocytes and endothelial cells  
and in the regulation of T cell receptor-mediated cell death.  
CC Mediated NF-kappa-B activation via the TRAF2/NIK pathway (By  
similarity).  
CC -!- SUBUNIT: Binds to TRAF1, TRAF2, and TRAF3, but not TRAF5 and  
TRAF6 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms A, B and  
C); secreted (isoform D).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=A;

CC Names=B; Sequence=Displayed;  
CC IsoId=O35714-2; Sequence=VSP\_006510;  
CC Names=C;  
CC IsoId=O35714-3; Sequence=VSP\_006511;  
CC Names=D;  
CC IsoId=O35714-4; Sequence=VSP\_006509;  
CC -!- TISSUE SPECIFICITY: Preferentially expressed in activated T  
lymphocytes.  
CC -!- INDUCTION: Upregulated in peripheral mononuclear cells after  
antigen stimulation/lymphocyte activation.  
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
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EMBL; U82534; AAB81243.1; --  
EMBL; AF109216; AAF14231.1; --  
EMBL; AF229432; AAF61566.1; --  
EMBL; AF229433; AAF61567.1; --  
EMBL; AF229434; AAF61568.1; --  
MGD; MGI:894675; Tnfrsf18.  
DR InterPro: IPR006210; IEFG.  
DR InterPro: IPR001368; TNFR\_c6.  
DR SMART; SM00181; EGF; 1.  
DR SMART; SM00208; TNFR; 2.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; FALSE NEG.  
DR PROSITE; PS00650; TNFR\_NGFR\_2; FALSE NEG.  
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
KW Alternative splicing.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 228 TUMOR NECROSIS FACTOR RECEPTOR  
FT DOMAIN 20 153 SUPERFAMILY MEMBER 18.  
FT TRANSMEM 154 174 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 175 228 POTENTIAL.  
FT REPEAT 28 61 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 62 101 TNFR-CYS 1.  
FT REPEAT 102 142 TNFR-CYS 2.  
FT DISULFID 29 44 BY SIMILARITY.  
FT DISULFID 62 74 BY SIMILARITY.  
FT DISULFID 69 82 BY SIMILARITY.  
FT DISULFID 103 122 BY SIMILARITY.  
FT DISULFID 116 141 BY SIMILARITY.  
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPLIC 121 228 NCSEQFTLTFPGKTHNAVCIPEPLTPEQYGHITVFLVM  
AACIFELTVGLHIVOLRHOHMCPTRETQPAFVOLSAD  
ACSFQPEEREGEOTEKCHLGGWRP -> KPAIRGGAVV  
S (in isoform D).  
FTTD=VSP\_006509.  
ETQPPAEVLSAEDACSFQPEEREGEOTEKCHLGGWRP .  
-> VLLQPSHSRCSCQLRLAASSSLRRNAGSRQKSVI  
WGVGHEAWSSVQPAKYKTCPAIPLVRAGAMLCITLPWAW  
PCSPQWRKVVYESGELRLGPMAAFLI (in isoform  
B).  
FTTD=VSP\_006510.  
ETQPPAEVLSAEDACSFQPEEREGEOTEKCHLGGWRP  
-> GOLCPREGENVSQAPHLQFYRDPAIRGGAVVS (in  
isoform C).  
FTTD=VSP\_006511.  
SQ SEQUENCE 228 AA; 25334 MW; 50D8C275D9C56259 CRC64;

Query Match 34.5%; Score 48; DB 1; Length 228;  
Best Local Similarity 40.0%; Pred. No. 5.3;  
Matches 10; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

```
QY 1 CREWTNCSLDGRSVLTKGTTEKDV 25
  ||||| : : :
Db 116 CRLWTNCSQGFELTTPGKNTHAV 140

RESULT 19
YCE8_YEAST STANDARD; PRT; 463 AA.
AC P25380;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Hypothetical SP52-like 52.0 kDa protein in APA1/DTP-PD11 intergenic
DE region.
GN YCLO48W OR YCLO48W.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Grenson M., Jauniaux J.-C., Urrestarazu L.A.;
RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: STRONG, TO YEAST SPORULATION-SPECIFIC PROTEIN 2
CC (SP52).
CC
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CC
DR EMBL; X59720; CAA42368.1; -
DR PIR; S19377; S19377.
DR Germonline; 138884; -
DR SGD; S0000553; YCLO48W.
DR InterPro; IPR000494; EGFR_L_domain.
DR Pfam; PF01030; Recep_L_domain; 1.
RW Hypothetical protein.
SQ SEQUENCE 463 AA; 52007 MW; DC84F0F4C16B1B59 CRC64;

Query Match 34.2%; Score 47.5; DB 1; Length 463;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 9; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 CRPWTNCSLDGRSVLTKGT 18
  ||||| :|||:
Db 378 CNKWTNPS-NGRSIRGG 394

RESULT 20
TNR3_MOUSE STANDARD; PRT; 415 AA.
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 3 precursor
DE (lymphotoxin-beta receptor).
GN LTR OR TNFRSF3 OR TNFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CVB; TISSUE=Lung;
RX MEDLINE=96072804; PubMed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.;

"Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
and expression."; J. Immunol. 155:5280-5288 (1995).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163885; PubMed=8586432;
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA Honjo T.;
RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
sequence trap and chromosomal mapping.";
RL Genomics 30:312-319 (1995).
[3]
RP INTERACTION WITH TRAF5.
RC STRAIN=BALB/c;
RX MEDLINE=96278943; PubMed=8663299;
RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
RA Yagita H., Okumura K.;
RT "TRAF5, an activator of NF-kappaB and putative signal transducer for
the lymphotoxin-beta receptor.";
RL J. Biol. Chem. 271:14661-14664 (1996).
CC -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC LTA and LTb, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
CC and TRAF5. May play a role in the development of lymphoid organs
CC (by similarity).
CC -1- SUBUNIT: Self-associates (By similarity). Associates with TRAF5.
CC Associates with TRAF3 and TRAF4 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
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CC
DR EMBL; U29173; AAA68964.1; -
DR EMBL; L38423; AAB00846.1; -
DR EMBL; U30798; AAA81334.1; -
DR HSP; O14763; IDOG.
DR MGD; MGI:104875; Ltbr.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00208; TNFR_C6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00652; TNFR_NGFR_2; 3.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 415
FT DOMAIN 31 223
FT TRANSMEM 224 244
FT DOMAIN 245 415
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 170
FT REPEAT 171 213
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 150
FT DISULFID 142 169
FT DISULFID 172 187
FT CARBOHYD 40 40
FT CARBOHYD 179 179
FT SEQUENCE 415 AA; 44956 MW; 29B326A56AEF661 CRC64;

Query Match 33.8%; Score 47; DB 1; Length 415;
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DR EMBL: X77156; CAA54399.1; -.
DR PIR: S41397; S41397; RNA_pol_DS_PS.
DR InterPro: IPR007095; RNA_pol_DS_PS.
KW Transferase; RNA-directed RNA polymerase.
SQ SEQUENCE 998 AA; 112187 MW; E9A64CE06555B21C CRC64;

Query Match 33.8%; Score 47; DB 1; Length 998;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNC 7
Db 262 CRPWTC 268

RESULT 24
TR18 HUMAN
ID TR18 HUMAN STANDARD; PRT; 241 AA.
AC Q9Y5U5; Q9Y5U5; Q9NYJ9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 18 precursor
DE (Glucocorticoid-induced TNFR-related protein) (Activation-inducible
DE TNFR family receptor).
DE TNFR family receptor).
GN TNFRSF18 OR GTR OR AITR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH TRAF1; TRAF2 AND
TRAF3.
RP RP TISSUE=Bone marrow;
RC MEDLINE=99175482; PubMed=10074429;
RA Gurney A.L., Masters S.A., Huang R.M., Pitti R.M., Mark D.T.,
RA Baldwin D.T., Gray A.M., Dowd A.D., Brush A.D., Heldens A.D.,
RA Schow A.D., Goddard A.D., Wood W.I., Baker K.P., Godowski P.J.,
RA Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family
RT and its receptor, a human ortholog of mouse GTR."
RL Curr. Biol. 9:215-218(1999).
RN [2]
SEQUENCE FROM N.A. (ISOFORM 1).
RP RP TISSUE=T-cell;
RC MEDLINE=99156876; PubMed=10037686;
RA Kwon B., Yu K.-Y., Ni J., Yu G.-L., Jang I.-K., Kim Y.-J., Xing L.,
RA Liu D., Wang S.-X., Kwon B.S.;
RT "Identification of a novel activation-inducible protein of the tumor
RT necrosis factor receptor superfamily and its ligand."
RL J. Biol. Chem. 274:6056-6061(1999).
RN [3]
SEQUENCE FROM N.A. (ISOFORM 2).
RP RP TISSUE=Thymus;
RC MEDLINE=20292073; PubMed=10836847;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Brunetti L., Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GTR."
RL Cell Death Differ. 7:408-410(2000).
CC CC -!- FUNCTION: Receptor for TNFSF18. Seems to be involved in
CC interactions between activated T lymphocytes and endothelial cells
CC and in the regulation of T cell receptor-mediated cell death.
CC Mediated NF-kappa-B activation via the TRAF2/NIK pathway.
CC CC -!- SUBUNIT: Binds to TRAF1, TRAF2, and TRAF3, but not TRAF5 and
CC TRAF6.
CC CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
CC Secreted (isoform 2).
CC CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9Y5U5-1; Sequence=Displayed;
CC Name=2; Synonyms=GTR-D;
CC IsoId=Q9Y5U5-2; Sequence=VSP_006508;
CC
```

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CC -!- TISSUE SPECIFICITY: Expressed in lymph node, peripheral blood
CC leukocytes and weakly in spleen.
CC -!- INDUCTION: Upregulated in peripheral mononuclear cells after
CC antigen stimulation/lymphocyte activation.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC
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CC
CC EMBL: AF125304; AAD22635.1; -.
CC EMBL: AF117297; AAD19694.1; -.
CC EMBL: AF241229; AAF63506.1; -.
CC Genew; HGNC:11914; TNFRSF18.
CC MIM; 603905; -.
CC GO; GO:0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.
CC GO; GO:0006916; P:anti-apoptosis; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro: IPR001368; TNFR_c6.
CC SMART; SM00208; TNFR_2.
CC PROSITE; PS00852; TNFR_NGFR_1; FALSE NEG.
CC PROSITE; PS00500; TNFR_NGFR_2; FALSE NEG.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Alternative splicing.
FT SIGNAL 1 25
FT CHAIN 26 241
FT DOMAIN 26 162
FT TRANSMEM 163 183
FT DOMAIN 184 241
FT REPEAT 34 72
FT REPEAT 74 112
FT REPEAT 115 153
FT DISULFID 34 49
FT DISULFID 74 86
FT DISULFID 81 94
FT DISULFID 115 134
FT DISULFID 128 153
FT CARBOHYD 146 146
FT VARSPLIC 135 241
FT
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 18.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT TNFR-CYS 1.
FT TNFR-CYS 2.
FT TNFR-CYS 3.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC...) (POTENTIAL).
FT TOFGFLTVPGNKTNAVCVPGSPAEPLGMLTVVLLAVAA
FT CULLITSAQLGHIKQLRSQCMWPRETOLLLEVPSTEDAR
FT SCOFFEERGERGSAEKGRLGLWV -> CWECRRERPKTE
FT AASSPRKSGASDRRRRGWETCCGCEPRGPPGPTAASPS
FT GAPQAGALRSALGALLFPWQOKWQEGSGDORPGPCSSAA
FT AAGPCRERETQSWPSSLAGPDGVGS (in isoform
FT 2).
FT FTId=VSP_006508.
FT CONFLICT 194 201 SOCMPRE -> K (IN REF. 2).
FT SEQUENCE 241 AA; 26000 MW; 90DC3B4AAVE82CBE CRC64;
Query Match 33.1%; Score 46; DB 1; Length 241;
Best Local Similarity 54.5%; Pred. No. 11;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDG 11
Db 128 CRPWTDCQFG 138

RESULT 25
CGH2_HSVSA
ID CGH2_HSVSA STANDARD; PRT; 254 AA.
AC Q01043;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclin homolog (V-cyclin).
GN 72 OR ECLF2.
OS Herpesvirus saimiri (strain 11).
```

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Gamaherpesvirinae; Rhadinovirus.  
OX NCBI\_TaxID=10383;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92333688; PubMed=1331287;  
RA Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,  
RA Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,  
RA Honess R.W.;  
RT "Primary structure of the herpesvirus saimiri genome.";  
RL J. Virol. 66:5047-5058(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92230228; PubMed=1314457;  
RA Nicholas J., Cameron K.R., Coleman H., Newman C., Honess R.W.;  
RT "Analysis of nucleotide sequence of the rightmost 43 kbp of  
RT herpesvirus saimiri (HVS) L-DNA: General conservation of genetic  
RT organization between HVS and Epstein-Barr virus.";  
RL Virology 188:296-310(1992).  
RN [3]  
RP SIMILARITY TO G-PROTEIN COUPLED RECEPTORS.  
RX MEDLINE=92115001; PubMed=1305943;  
RA Nicholas J., Cameron K.R., Honess R.W.;  
RT "Herpesvirus saimiri encodes homologues of G protein-coupled  
RT receptors and cyclins.";  
RL Nature 355:362-365(1992).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (3.00 ANGSTROMS) OF 22-250.  
RX MEDLINE=99197290; PubMed=10368294;  
RA Schulze-Gahmen U., Jung J.U., Kim S.-H.;  
RT "Crystal structure of a viral cyclin, a positive regulator of cyclin-  
RT dependent kinase 6.";  
RL Structure 7:245-254(1999).  
CC -!- FUNCTION: MAY BE HIGHLY RELEVANT TO THE PROCESS OF CELLULAR  
CC TRANSFORMATION AND RAPID T-CELL PROLIFERATION EFFECTED BY HVS  
CC DURING LATENT INFECTIONS OF T-CELLS IN SUSCEPTIBLE HOSTS.  
CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.  
CC  
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CC  
CC EMBL; S76368; AAB21115.1; -;  
DR EMBL; X64346; CAA45695.1; -;  
DR EMBL; M86409; AAB46148.1; -;  
DR PDB; 1B02; 15-JUN-99.  
DR PDB; 1UCW; 27-FEB-02.  
DR InterPro; IPR006670; Cyclin.  
DR InterPro; IPR006671; Cyclin\_N.  
DR Pfam; PF00134; cyclin; 1.  
DR SMART; SM00385; CYCLIN; 1.  
DR PROSITE; PS00292; CYCLIN; 1.  
KW Cyclin; Cell cycle; Cell division; 3D-structure.  
FT HELIX 24 29  
FT TURN 30 32  
FT TURN 30 32  
FT TURN 40 43  
FT TURN 40 43  
FT HELIX 49 65  
FT TURN 66 67  
FT TURN 70 71  
FT HELIX 72 83  
FT TURN 84 86  
FT TURN 91 93  
FT TURN 94 108  
FT HELIX 116 121  
FT TURN 122 125  
FT TURN 129 142  
FT TURN 143 145  
FT HELIX 152 155  
FT HELIX 156 162

FT TURN 163 164  
FT TURN 167 168  
FT HELIX 170 184  
FT TURN 185 186  
FT TURN 188 189  
FT TURN 190 192  
FT HELIX 195 209  
FT TURN 210 210  
FT TURN 216 216  
FT HELIX 217 220  
FT HELIX 221 223  
FT TURN 224 226  
FT HELIX 230 242  
FT TURN 243 244  
FT HELIX 247 249  
SQ SEQUENCE 254 AA; 28637 MW; B682EB1011207F4 CRC64;  
Query Match 33.1%; Score 46; DB 1; Length 254;  
Best Local Similarity 44.8%; Pred. No. 12;  
Matches 13; Conservative 1; Mismatches 11; Indels 4; Gaps 1;  
QY 1 CRPWTNCSLDGRSVLKTGT----TEKVVV 25  
DB 214 CRPWTCTLEDLSILNFSNTVTRTKDQV 242  
RESULT 26  
ASG2\_ECOLI STANDARD; PRT; 348 AA.  
ID ASG2\_ECOLI  
AC P00805;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE L-asparaginase II precursor (EC 3.5.1.1) (L-asparagine  
DE amidohydrolase II) (L-ASNase II) (Colaspase).  
GN ANSB OR B2957.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90170867; PubMed=2407723;  
RA Jennings M.P., Beacham I.R.;  
RT "Analysis of the Escherichia coli gene encoding L-asparaginase II,  
RT ansB, and its regulation by cyclic AMP receptor and FNR proteins.";  
RL J. Bacteriol. 172:1491-1498(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=90382683; PubMed=2144836;  
RA Bonthron D.T.;  
RT "L-asparaginase II of Escherichia coli K-12: cloning, mapping and  
RT sequencing of the ansB gene.";  
RL Gene 91:101-105(1990).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1232-1244(1997).  
RN [4]  
RP SEQUENCE OF 23-348.  
RX MEDLINE=80135739; PubMed=6766894;  
RA Maiba T., Matsuda G.;  
RT "The primary structure of L-asparaginase from Escherichia coli.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 361:105-117(1980).  
RN [5]  
RP PARTIAL SEQUENCE.

RX MEDLINE=80048329; PubMed=387570;  
RA Maita T., Morokuma K., Matsuda G.;  
RT "Amino acid sequences of the tryptic peptides from carboxymethylated  
RT L-asparaginase from *Escherichia coli*.";  
RL Hoppe-Sejler's Z. Physiol. Chem. 360:1483-1495(1979).  
RN [6]  
RN ACTIVE SITE.  
RX MEDLINE=77140944; PubMed=321449;  
RA Peterson R.G., Richards P.F., Handschumacher R.E.;  
RT "Structure of peptide from active site region of *Escherichia coli* L-  
RT asparaginase.";  
RL J. Biol. Chem. 252:2072-2076(1977).  
RN [7]  
RN SUBUNITS.  
RX MEDLINE=73007901; PubMed=4561256;  
RA Greenquist A.C., Wriston J.C. Jr.;  
RT "Chemical evidence for identical subunits in L-asparaginase from  
RT *Escherichia coli* B.";  
RL Arch. Biochem. Biophys. 152:280-286(1972).  
RN [8]  
RN ACTIVE SITE THR-34.  
RX MEDLINE=91293312; PubMed=1906013;  
RA Harms E., Wehner A., Aung H.P., Roehm K.H.;  
RT "A catalytic role for threonine-12 of *E. coli* asparaginase II as  
RT established by site-directed mutagenesis.";  
RL FEBS Lett. 285:55-58(1991).  
RN [9]  
RN MUTAGENESIS OF HISTIDINE RESIDUES.  
RX MEDLINE=92394146; PubMed=1521538;  
RA Wehner A., Harms E., Jennings M.P., Beacham I.R., Derst C., Bast P.,  
RA Roehm K.H.;  
RT "Site-specific mutagenesis of *Escherichia coli* asparaginase II. None  
RT of the three histidine residues is required for catalysis.";  
RL Eur. J. Biochem. 208:475-480(1992).  
RN [10]  
RN MUTAGENESIS OF THREONINE AND SERINE RESIDUES.  
RX MEDLINE=93165634; PubMed=1287659;  
RA Ders C., Henseling J., Roehm K.H.;  
RT "Probing the role of threonine and serine residues of *E. coli*  
RT asparaginase II by site-specific mutagenesis.";  
RL Protein Eng. 5:785-789(1992).  
RN [11]  
RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).  
RX MEDLINE=93165718; PubMed=8434007;  
RA Swain A.L., Jaskolski M., Housset D., Rao J.K.M., Wlodawer A.;  
RT "Crystal structure of *Escherichia coli* L-asparaginase, an enzyme used  
RT in cancer therapy.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:1474-1478(1993).  
RN [12]  
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT VAL-111.  
RX MEDLINE=96305806; PubMed=8706882;  
RA Palm G.J., Lubkowski J., Derst C., Schleper S., Roehm K.H.,  
RA Wlodawer A.;  
RT "A covalently bound catalytic intermediate in *Escherichia coli*  
RT asparaginase: crystal structure of a Thr-89-Val mutant.";  
RL FEBS Lett. 390:211-216(1996).  
CC -1- CATALYTIC ACTIVITY: L-asparagine + H(2)O = L-aspartate + NH(3).  
CC -1- SUBUNIT: Homotetramer.  
CC -1- SUBCELLULAR LOCATION: Periplasmic.  
CC -1- INDUCTION: BY CAMP AND ANAEROBIOSIS.  
CC -1- PHARMACEUTICAL: Available under the names Crastinin (Bayer),  
CC Elspar (Merck), Kidrolase (Rhône-Poulenc) and Leunase (Kycwa).  
CC Also available as a PEG-conjugated form (pegasparase) under the  
CC name Oncaspar (Erzon). Used as an antineoplastic in chemotherapy.  
CC Reduces the quantity of asparagine available to cancer cells.  
CC -1- MISCELLANEOUS: KM = 1.15 X 10<sup>-5</sup> M.  
CC -1- MISCELLANEOUS: *E. coli* CONTAINS TWO L-ASPARAGINASE ISOENZYMES:  
CC L-ASPARAGINASE I, A LOW-AFFINITY ENZYME LOCATED IN THE CYTOPLASM,  
CC AND L-ASPARAGINASE II, A HIGH-AFFINITY SECRETED ENZYME.  
CC -1- SIMILARITY: Belongs to the asparaginase 1 family.  
CC -1- DATABASE: NAME-Worthington enzyme manual;  
CC WWW="http://www.worthington-biochem.com/ASPR/".  
-----

CC CC MEDLINE=80048329; PubMed=387570;  
CC RA Maita T., Morokuma K., Matsuda G.;  
CC RT "Amino acid sequences of the tryptic peptides from carboxymethylated  
CC RT L-asparaginase from *Escherichia coli*.";  
CC RL Hoppe-Sejler's Z. Physiol. Chem. 360:1483-1495(1979).  
CC RN [6]  
CC RN ACTIVE SITE.  
CC RX MEDLINE=77140944; PubMed=321449;  
CC RA Peterson R.G., Richards P.F., Handschumacher R.E.;  
CC RT "Structure of peptide from active site region of *Escherichia coli* L-  
CC RT asparaginase.";  
CC RL J. Biol. Chem. 252:2072-2076(1977).  
CC RN [7]  
CC RN SUBUNITS.  
CC RX MEDLINE=73007901; PubMed=4561256;  
CC RA Greenquist A.C., Wriston J.C. Jr.;  
CC RT "Chemical evidence for identical subunits in L-asparaginase from  
CC RT *Escherichia coli* B.";  
CC RL Arch. Biochem. Biophys. 152:280-286(1972).  
CC RN [8]  
CC RN ACTIVE SITE THR-34.  
CC RX MEDLINE=91293312; PubMed=1906013;  
CC RA Harms E., Wehner A., Aung H.P., Roehm K.H.;  
CC RT "A catalytic role for threonine-12 of *E. coli* asparaginase II as  
CC RT established by site-directed mutagenesis.";  
CC RL FEBS Lett. 285:55-58(1991).  
CC RN [9]  
CC RN MUTAGENESIS OF HISTIDINE RESIDUES.  
CC RX MEDLINE=92394146; PubMed=1521538;  
CC RA Wehner A., Harms E., Jennings M.P., Beacham I.R., Derst C., Bast P.,  
CC RA Roehm K.H.;  
CC RT "Site-specific mutagenesis of *Escherichia coli* asparaginase II. None  
CC RT of the three histidine residues is required for catalysis.";  
CC RL Eur. J. Biochem. 208:475-480(1992).  
CC RN [10]  
CC RN MUTAGENESIS OF THREONINE AND SERINE RESIDUES.  
CC RX MEDLINE=93165634; PubMed=1287659;  
CC RA Ders C., Henseling J., Roehm K.H.;  
CC RT "Probing the role of threonine and serine residues of *E. coli*  
CC RT asparaginase II by site-specific mutagenesis.";  
CC RL Protein Eng. 5:785-789(1992).  
CC RN [11]  
CC RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).  
CC RX MEDLINE=93165718; PubMed=8434007;  
CC RA Swain A.L., Jaskolski M., Housset D., Rao J.K.M., Wlodawer A.;  
CC RT "Crystal structure of *Escherichia coli* L-asparaginase, an enzyme used  
CC RT in cancer therapy.";  
CC RL Proc. Natl. Acad. Sci. U.S.A. 90:1474-1478(1993).  
CC RN [12]  
CC RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT VAL-111.  
CC RX MEDLINE=96305806; PubMed=8706882;  
CC RA Palm G.J., Lubkowski J., Derst C., Schleper S., Roehm K.H.,  
CC RA Wlodawer A.;  
CC RT "A covalently bound catalytic intermediate in *Escherichia coli*  
CC RT asparaginase: crystal structure of a Thr-89-Val mutant.";  
CC RL FEBS Lett. 390:211-216(1996).  
CC -1- CATALYTIC ACTIVITY: L-asparagine + H(2)O = L-aspartate + NH(3).  
CC -1- SUBUNIT: Homotetramer.  
CC -1- SUBCELLULAR LOCATION: Periplasmic.  
CC -1- INDUCTION: BY CAMP AND ANAEROBIOSIS.  
CC -1- PHARMACEUTICAL: Available under the names Crastinin (Bayer),  
CC Elspar (Merck), Kidrolase (Rhône-Poulenc) and Leunase (Kycwa).  
CC Also available as a PEG-conjugated form (pegasparase) under the  
CC name Oncaspar (Erzon). Used as an antineoplastic in chemotherapy.  
CC Reduces the quantity of asparagine available to cancer cells.  
CC -1- MISCELLANEOUS: KM = 1.15 X 10<sup>-5</sup> M.  
CC -1- MISCELLANEOUS: *E. coli* CONTAINS TWO L-ASPARAGINASE ISOENZYMES:  
CC L-ASPARAGINASE I, A LOW-AFFINITY ENZYME LOCATED IN THE CYTOPLASM,  
CC AND L-ASPARAGINASE II, A HIGH-AFFINITY SECRETED ENZYME.  
CC -1- SIMILARITY: Belongs to the asparaginase 1 family.  
CC -1- DATABASE: NAME-Worthington enzyme manual;  
CC WWW="http://www.worthington-biochem.com/ASPR/".  
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EMBL; M34277; AAA24062.1; -;  
EMBL; M34234; AAA23445.1; -;  
EMBL; U28377; AAA69124.1; -;  
EMBL; AE000378; AAC75994.1; -;  
PIR; A35132; XDEC.  
PDB; 3ECA; 31-OCT-93.  
PDB; 4ECA; 16-JUN-97.  
PDB; 1HO3; 07-MAR-01.  
EcGene; EG10046; ansB  
InterPro; IPR004550; AsnASE\_II.  
InterPro; IPR006034; Asp/Glutamase.  
Pfam; PF00710; Asparaginase; 1.  
PRINTS; PR00139; ASGNLASE.  
ProDom; PD003221; Asp/Glutamase; 1.  
TIGRfams; TIGR00520; asnASE\_II; 1.  
PROSITE; PS00144; ASN\_GLN\_ASE\_1; 1.  
PROSITE; PS00917; ASN\_GLN\_ASE\_2; 1.  
Hydrolase; Signal; Periplasmic; Pharmaceutical; 3D-structure;  
KW Complete proteome.  
FT SIGNAL 1 22  
FT CHAIN 23 348 L-ASPARAGINASE II.  
FT ACT\_SITE 34 34  
FT ACT\_SITE 111 111 BY SIMILARITY.  
FT ACT\_SITE 112 112 BY SIMILARITY.  
FT ACT\_SITE 184 184 BY SIMILARITY.  
FT DISULFID 99 127  
FT BINDING 141 141  
FT MUTAGEN 34 34  
FT CONFLICT 49 49  
FT CONFLICT 86 86  
FT CONFLICT 132 132 MISSING (IN REF. 4).  
FT CONFLICT 156 156 MISSING (IN REF. 4).  
FT CONFLICT 171 171 MISSING (IN REF. 4).  
FT CONFLICT 206 206 N -> D (IN REF. 4).  
FT CONFLICT 268 268 N -> D (IN REF. 4).  
FT CONFLICT 274 274 S -> T (IN REF. 4).  
FT CONFLICT 285 285 T -> D (IN REF. 4).  
FT CONFLICT 290 290 MISSING (IN REF. 4).  
FT CONFLICT 330 330 MISSING (IN REF. 4).  
FT STRAND 25 32  
FT TURN 34 36  
FT STRAND 38 38  
FT STRAND 48 48  
FT HELIX 54 59  
FT TURN 60 60  
FT TURN 62 63  
FT HELIX 64 66  
FT TURN 67 67  
FT STRAND 69 78  
FT HELIX 80 82  
FT HELIX 85 99  
FT TURN 100 101  
FT STRAND 104 108  
FT TURN 112 113  
FT HELIX 114 124  
FT STRAND 131 134  
FT TURN 140 141  
FT TURN 143 144  
FT TURN 147 159  
FT HELIX 161 163  
FT TURN 164 165  
FT STRAND 169 172  
FT TURN 173 174  
FT STRAND 175 178  
FT TURN 179 181  
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FT STRAND 182 184  
 FT STRAND 186 186  
 FT TURN 190 191  
 FT STRAND 193 195  
 FT TURN 196 198  
 FT STRAND 202 205  
 FT TURN 206 207  
 FT STRAND 208 211  
 FT HELIX 220 222

Query Match 33.1%; Score 46; DB 1; Length 348;  
 Best Local Similarity 69.2%; Pred. No. 17;  
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 LDGRSVLTGTTE 21  
 |||||  
 DB 177 LDGRDVTNTTD 189

## RESULT 27

KHSE\_CORGL STANDARD; PRT; 308 AA.

AC P07128; P08210;  
 DT 01-APR-1988 (Rel. 07, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Homoserine kinase (EC 2.7.1.39) (HK).  
 GN THRB OR CGL1184.  
 OS Corynebacterium glutamicum (Brevibacterium flavum).  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
 OX NCBI\_TaxID=1718;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-10.  
 RC STRAIN=ATCC 13059 / AS019;  
 RX MEDLINE=88216182; PubMed=2835591;  
 RA Peoples O.P., Liebl W., Bodis M., Maeng P.J., Follett M.T.,  
 RA Archer J.A.C., Sinskey A.J.;  
 RT "Nucleotide sequence and fine structural analysis of the  
 RT Corynebacterium glutamicum hom-thrB operon.";  
 RL Mol. Microbiol. 2:63-72(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 13869;  
 RX MEDLINE=87231082; PubMed=3035505;  
 RA Mateos L.M., del Real G., Aguilar A., Martin J.F.;  
 RT "Nucleotide sequence of the homoserine kinase (thr B) gene of  
 RT Brevibacterium lactofermentum.";  
 RL Nucleic Acids Res. 15:3922-3922(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;  
 RX Nakagawa S.;  
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";  
 RL Submitted (MAY-2002) to the ENBL/GenBank/DBJ databases.  
 CC -!- CATALYTIC ACTIVITY: ATP + L-homoserine = ADP + O-phospho-L-homoserine.  
 CC -!- PATHWAY: Threonine biosynthesis from aspartate; fourth step.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -!- SIMILARITY: Belongs to the GMP kinase family. Homoserine kinase subfamily.

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DR EMBL; Y00546; CAA68615.1; -  
 DR EMBL; Y00140; CAA68332.1; -  
 DR EMBL; AP005277; BAB98577.1; -

DR PIR; S00866; KIFKMG.  
 DR HAMAP; MF\_00384; -; 1.  
 DR InterPro; IPR006204; GHMP\_kinase.  
 DR InterPro; IPR006203; GHMPKase ATP.  
 DR InterPro; IPR000870; Homoser\_Kin.  
 DR Pfam; PF00288; GHMP\_kinases; 1.  
 DR PRINTS; PR00958; HOMSERKINASE.  
 DR TIGRFAMs; TIGR00191; thrB; 1.  
 DR PROSITE; PS00627; GHMP\_KINASES ATP; 1.  
 KW Threonine biosynthesis; Transferase; Kinase; ATP-binding;  
 KW Complete proteome.  
 FT INIT MET 0  
 FT NP BIND 94 104 ATP (POTENTIAL).  
 FT CONFLICT 245 245 I -> V (IN REF. 2).  
 FT CONFLICT 245 245 I -> V (IN REF. 2).  
 SQ SEQUENCE 308 AA; 32489 MW; 492AF795C012623 CRC64;

Query Match 32.4%; Score 45; DB 1; Length 308;  
 Best Local Similarity 70.0%; Pred. No. 21;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WTNCSDLGDS 13  
 |||||  
 DB 152 WTNLSDGKS 161

## RESULT 28

TL1B\_HUMAN STANDARD; PRT; 401 AA.

AC 000300; O60236; Q9UHP4;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 11B precursor  
 DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).  
 GN TNFRSF11B OR OPG OR OCIF.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=97262071; PubMed=9108485;  
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
 RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,  
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,  
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
 RA Suggs S., Boyle W.J.;  
 RT "Osteoprotegerin: a novel secreted protein involved in the regulation  
 RT of bone density.";  
 RL Cell 89:309-319(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=lung cancer;  
 RX MEDLINE=98151033; PubMed=9492069;  
 RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,  
 RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,  
 RA Tsuda E., Morinaga T., Higashio K.;  
 RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and  
 RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits  
 RT osteoclastogenesis in vitro.";  
 RL Endocrinology 139:1329-1337(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND VARIANT ASN-3.  
 RC TISSUE=Placenta;  
 RX MEDLINE=98351569; PubMed=9688283;  
 RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;  
 RT "Cloning and characterization of the gene encoding human  
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";  
 RL Eur. J. Biochem. 254:685-691(1998).  
 RN [4]  
 RP SEQUENCE FROM N.A., AND VARIANT ASN-3.



CC RX MEDLINE=9238257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins K.F., Jordan H., Moore I., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., 15,000 full-length  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[5]  
RN SEQUENCE OF 22-36 AND 378-401.  
RP MEDLINE=98238645; PubMed=9571159;  
RX Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,  
RA Morinaga T., Tsuda E., Higashio K.;  
RT "Characterization of monomeric and homodimeric forms of  
osteoclastogenesis inhibitory factor.";  
RL Biochem. Biophys. Res. Commun. 245:382-387(1998).  
[6]  
RN SEQUENCE OF 22-393 FROM N.A.  
RP TISSUE=Placenta;  
RC He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-P.;  
RT "Cloning and expression of osteoprotegerin from Homo sapiens.";  
RL Acta Biochim. Biophys. Sin. 31:680-684(1999).  
[7]  
RN SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.  
RP MEDLINE=97312536; PubMed=9168977;  
RX Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,  
RA Morinaga T., Higashio K.;  
RT "Isolation of a novel cytokine from human fibroblasts that  
specifically inhibits osteoclastogenesis.";  
RL Biochem. Biophys. Res. Commun. 234:137-142(1997).  
[8]  
RN TRAIL BINDING.  
RP MEDLINE=98269100; PubMed=9603945;  
RX Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,  
RA Dul E., Appelbaum E.R., Eichman C., DiPrinzio R., Dodds R.A.,  
RA James I.E., Rosenberg M., Lee J.C., Young P.R.;  
RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";  
RL J. Biol. Chem. 273:14363-14367(1998).  
[9]  
RN CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.  
RP MEDLINE=98148058; PubMed=9478964;  
RX Yamaguchi K., Kinoshita M., Goto M., Kobayashi F., Tsuda E.,  
RA Morinaga T., Higashio K.;  
RT "Characterization of structural domains of human osteoclastogenesis  
inhibitory factor.";  
RL J. Biol. Chem. 273:5117-5123(1998).  
[10]  
RN REVIEW.  
RP MEDLINE=21395914; PubMed=11505389;  
RX Hofbauer L.C., Neubauer A., Heufelder A.E.;  
RT "Receptor activator of nuclear factor-kappaB ligand and  
osteoprotegerin: potential implications for the pathogenesis and  
treatment of malignant bone diseases.";  
RL Cancer 92:460-470(2001).  
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes  
its function in osteoclastogenesis. Inhibits the activation of  
osteoclasts and promotes osteoclast apoptosis in vitro. Bone  
homeostasis seems to depend on the local RANKL/OPG ratio. May also  
play a role in preventing arterial calcification. May act as decoy

receptor for TRAIL and protect against apoptosis. TRAIL binding  
blocks the inhibition of osteoclastogenesis.  
-!- SUBUNIT: Homodimer.  
-!- SUBCELLULAR LOCATION: Secreted.  
-!- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,  
liver, spleen, thymus, prostate, ovary, small intestine, thyroid,  
lymph node, trachea, adrenal gland, testis and bone marrow.  
Detected at very low levels in brain, placenta and skeletal  
muscle. Highly expressed in fetal kidney, liver and lung.  
-!- INDUCTION: Upregulated by increasing calcium-concentration in the  
medium and estrogens. Downregulated by glucocorticoids.  
-!- PTM: N-glycosylated. Contains sialic acid residues.  
-!- PTM: The N-terminus is blocked.  
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
-!- SIMILARITY: Contains 2 death domains.  
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CC EMBL; U94332; AAB53709.1; -  
DR EMBL; AB002146; BAA25910.1; -  
DR EMBL; AB008822; BAA32076.1; -  
DR EMBL; AB008821; BAA32076.1; JOINED.  
DR EMBL; BC030155; AAH30155.1; -  
DR EMBL; AF134187; AAF20168.1; -  
DR HSSP; P25942; 1CDF.  
DR Genew; HGNC:11909; TNFRSF11B.  
DR MIM; 602643; -; C:extracellular; TAS.  
DR GO; GO:0005576; C:extracellular; TAS.  
DR GO; GO:0003125; P:cytokine activity; TAS.  
DR GO; GO:0004872; P:receptor activity; TAS.  
DR GO; GO:0007165; P:signal transduction; TAS.  
DR GO; GO:0001501; P:skeletal development; TAS.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS00117; DEATH\_DOMAIN; FALSE\_NEG.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS00650; TNFR\_NGFR\_2; 2.  
KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.  
FT SIGNAL 1 21  
FT CHAIN 22 401 TUMOR NECROSIS FACTOR RECEPTOR  
FT REPEAT 24 62 SUPERFAMILY MEMBER 11B.  
FT REPEAT 65 105 TNFR-CYS 1.  
FT REPEAT 107 142 TNFR-CYS 2.  
FT REPEAT 145 185 TNFR-CYS 3.  
FT REPEAT 198 289 TNFR-CYS 4.  
FT DOMAIN 270 385 DEATH 1.  
FT SITE 400 400 DEATH 2.  
FT SITE 400 400 INVOLVED IN DIMERIZATION.  
FT DISULFID 41 54 BY SIMILARITY.  
FT DISULFID 44 62 BY SIMILARITY.  
FT DISULFID 65 80 BY SIMILARITY.  
FT DISULFID 83 97 BY SIMILARITY.  
FT DISULFID 87 105 BY SIMILARITY.  
FT DISULFID 107 118 BY SIMILARITY.  
FT DISULFID 124 142 BY SIMILARITY.  
FT DISULFID 145 160 BY SIMILARITY.  
FT DISULFID 166 185 BY SIMILARITY.  
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARIANT 3 3 K -> N.  
/FTId=VAR\_013439.

FT MUTAGEN 400 400 C->S: ABOLISHES DIMERIZATION.  
 FT MUTAGEN 400 401 MISSING: ABOLISHES DIMERIZATION.  
 FT CONFLICT 263 263 D->A (IN REF. 1).  
 SQ SEQUENCE 401 AA; 46040 MW; EDF448B67D86C71E CRC64;  
 Query Match 32.4%; Score 45; DB 1; Length 401;  
 Best Local Similarity 39.1%; Pred. No. 28;  
 Matches 9; Conservative 3; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 CREWTNCSLDGRSVLKTGTTEKD 23  
 DB 160 CRKHTNCSVGLLLTQKGNATHD 182  
 ID T11B RAT STANDARD; PRT; 401 AA.  
 AC Q08727;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Tumor necrosis factor receptor superfamily member 11B precursor  
 DE (Osteoprotegerin).  
 GN TNRFR11B OR OPG.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryonic intestine;  
 RX MEDLINE=97262071; PubMed=9108485;  
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
 RA Luehly R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,  
 RA Derese M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,  
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
 RA Suggs S., Boyle W.J.  
 RA "Osteoprotegerin: a novel secreted protein involved in the regulation  
 RT of bone density.";  
 RT Cell 89:309-319(1997).  
 RL CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes  
 CC its function in osteoclastogenesis. Inhibits the activation of  
 CC osteoclasts and promotes osteoclast apoptosis. Bone homeostasis  
 CC seems to depend on the local RANKL/OPG ratio. May also play a role  
 CC in preventing arterial calcification. May act as decoy receptor  
 CC for TRAIL and protect against apoptosis. TRAIL binding blocks the  
 CC inhibition of osteoclastogenesis (By similarity).  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -!- INDUCTION: Upregulated by osteopontin.  
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -!- SIMILARITY: Contains 2 death domains.  
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 CC -----  
 CC EMBL; U94330; AAB53707.1; -  
 CC HSSP; P25942; 1CDF.  
 CC InterPro; IPR000488; Death.  
 CC InterPro; IPR001368; TNFR\_c6.  
 CC Pfam; PF00020; TNFR\_c6; 4.  
 CC SMART; SM00005; DEATH; 1.  
 CC SMART; SM00208; TNFR; 4.  
 CC PROSITE; PS0017; DEATH\_DOMAIN; FALSE\_NEG.  
 CC PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 CC PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
 CC Cytokine; Apoptosis; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 21 BY SIMILARITY.  
 FT CHAIN 22 401 TUMOR NECROSIS FACTOR RECEPTOR  
 FT SUPERFAMILY MEMBER 11B.  
 FT REPEAT 24 62 TNFR-CYS 1.  
 FT REPEAT 65 105 TNFR-CYS 2.  
 FT REPEAT 107 142 TNFR-CYS 3.  
 FT REPEAT 145 185 TNFR-CYS 4.  
 FT DOMAIN 198 269 DEATH 1.  
 FT DOMAIN 270 365 DEATH 2.  
 FT SITE 400 400 INVOLVED IN DIMERIZATION (BY SIMILARITY).  
 FT DISULFID 41 54 BY SIMILARITY.  
 FT DISULFID 44 62 BY SIMILARITY.  
 FT DISULFID 65 80 BY SIMILARITY.  
 FT DISULFID 83 97 BY SIMILARITY.  
 FT DISULFID 87 105 BY SIMILARITY.  
 FT DISULFID 107 118 BY SIMILARITY.  
 FT DISULFID 124 142 BY SIMILARITY.  
 FT DISULFID 145 160 BY SIMILARITY.  
 FT DISULFID 166 185 BY SIMILARITY.  
 FT CARBOHYD 98 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 165 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 178 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 289 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 401 AA; 46192 MW; FECSA31FD4E573A CRC64;  
 Query Match 32.4%; Score 45; DB 1; Length 401;  
 Best Local Similarity 40.0%; Pred. No. 28;  
 Matches 10; Conservative 3; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 CREWTNCSLDGRSVLKTGTTEKD 25  
 DB 160 CRKHTNCSVGLLLTQKGNATHD 184  
 ID RBAL CAEEL STANDARD; PRT; 412 AA.  
 AC P90917;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Trp-Asp repeats containing protein RBA-1.  
 GN RBA-1 OR K07A1.11.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Percy C.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: Contains 6 WD repeats.  
 CC -!- SIMILARITY: Belongs to the WD-repeat RBAP46/RBAP48/MSI1 family.  
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 CC -----  
 CC EMBL; Z81097; CAB03172.1; -  
 CC PIR; T23385; T23385.  
 CC WormPep; K07A1.11; CE11860.  
 CC InterPro; IPR001680; WD40.  
 CC Pfam; PF04000; WD40; 5.  
 CC PRINTS; PR00320; GPROTEINRPT.  
 CC SMART; SM00320; WD40; 5.  
 CC PROSITE; PS00678; WD\_REPEATS\_1; 2.  
 CC PROSITE; PS00082; WD\_REPEATS\_2; 4.  
 CC PROSITE; PS50294; WD\_REPEATS\_REGION; 1.

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KW Repeat; WD repeat.
FT REPEAT 117 157 WD 1.
FT REPEAT 169 209 WD 2.
FT REPEAT 219 259 WD 3.
FT REPEAT 262 302 WD 4.
FT REPEAT 306 346 WD 5.
FT REPEAT 365 405 WD 6.
SQ SEQUENCE 412 AA; 46691 MW; 7f657a7f4f2d7772 CRC64;

Query Match 32.4%; Score 45; DB 1; Length 412;
Best Local Similarity 37.5%; Pred. No. 29;
Matches 9; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

Qy 2 RPWTNCSLDGRSVLKTGTTEKDV 25
Dy 379 RPWTNCSDEFNALQVWVENSIV 402

RESULT 31
TR21 MOUSE STANDARD; PRT; 655 AA.
AC Q9EP05; Q91W77; Q91XH9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-
DE related death receptor-6) (Death receptor 6).
GN TNFRSP21 OR DR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Kidney;
RA Isogai D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F.,
RA Minami M.;
RT "Mouse DR6: mouse homolog of human TNFR-related death receptor-6
RT (DR6).";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Kidney;
RA Kim V., Machleidt T., Shi W.-X., Wang X., Cai Z.;
RA "Murine DR6: murine TNFR-related death receptor-6";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; Pubmed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whitting J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP FUNCTION.
RX MEDLINE=21571606; Pubmed=11714751;
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RA Zhao H., Yan M., Wang H., Erickson S., Grewal I.S., Dixit V.M.;
RT "Impaired c-Jun amino terminal kinase activity and T cell
RT differentiation in death receptor 6-deficient mice.";
RL J. Exp. Med. 194:1441-1448(2001).
CC -!- FUNCTION: May activate NF-kappa-B and promote apoptosis (By
CC similarity). May activate JNK and be involved in T-cell
CC differentiation.
CC -!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
CC May be involved in T-cell differentiation.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in adult spleen,
CC thymus, testis, prostate, ovary, small intestine, colon, brain,
CC lung and kidney, and in fetal brain, liver and lung. Detected at
CC lower levels in adult peripheral blood leukocytes, lung, and in
CC fetal muscle, heart, kidney, small intestine and skin. Detected in
CC T-cells, B-cells and monocytes. In T-cells expression is highest
CC in Th0 cells, intermediate in Th2 cells and lower in Th1 cells.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-25 is the initiator.
CC -----
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CC -----
CC EMBL; AF322069; AAG38115.1; -
CC EMBL; AY043489; AAK74193.1; -
CC EMBL; BC016420; AAH16420.1; -
CC HSSP; O14763; 1DOG.
CC MGD; MGI:2151075; Tnfrsf21.
CC InterPro; IPR000488; Death.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00531; Death; 1.
CC Pfam; PF00020; TNFR_c6; 4.
CC SMART; SM00005; DEATH; 1.
CC SMART; SM00208; TNFR; 4.
CC PROSITE; PS50017; DEATH_DOMAIN; 1.
CC PROSITE; PS00852; TNFR_NGFR_1; 1.
CC PROSITE; PS50050; TNFR_NGFR_2; 1.
CC PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 41
FT CHAIN 42 655
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 21.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT DEATH.
FT TNFR-CYS 1.
FT TNFR-CYS 2.
FT TNFR-CYS 3.
FT TNFR-CYS 4.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT W -> L (IN REF. 1).
FT M -> I (IN REF. 3).
FT CONFLICT 352 523
FT SEQUENCE 655 AA; 71982 MW; 5EC7C51C7C99EFF7 CRC64;
```



DR PRINTS; PRO1349; WNTPROTEIN.  
 DR SNART; SMO0097; WNT1; 1.  
 DR PROSITE; PS00246; WNT1; 1.  
 KW Wnt signaling pathway; Developmental protein; Glycoprotein; Signal.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT CHAIN 23 357 WNT-9B PROTEIN.  
 FT CARBOHYD 99 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 357 AA; 38970 MW; E1221629A0294CB6 CRC64;

Query Match 31.7%; Score 44; DB 1; Length 357;  
 Best Local Similarity 57.9%; Pred. No. 36;  
 Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 2;

QY 4 WNTCSLDGRS-VLKTTGTE 21  
 DB 98 W-NCSLEGRGTLKRGFK 115

RESULT 34  
 LEU3\_BUCUE  
 ID LEU3\_BUCUE STANDARD; PRT; 364 AA.  
 AC Q9EVH5;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 3-isopropylmalate dehydrogenase (EC 1.1.1.85) (Beta-IPM dehydrogenase)  
 DE (IMDH) (3-IPM-DH).  
 GN LEUB.  
 OS Buchnera aphidicola (subsp. Uroleucon erigeronensis).  
 OG Plasmid pLeu (pEap1).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Buchnera.  
 OX NCBI\_TaxID=168385;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20576185; PubMed=11133977;  
 RA Wernegreen J.J.; Moran N.A.;  
 RT "Vertical transmission of biosynthetic plasmids in aphid endosymbionts (Buchnera).";  
 RL J. Bacteriol. 183:785-790 (2001).  
 CC -!- FUNCTION: Catalyzes the oxidation of 3-carboxy-2-hydroxy-4-methylpentanoate (3-isopropylmalate) to 3-carboxy-4-methyl-2-oxopentanoate. The product decarboxylates to 4-methyl-2-oxopentanoate.  
 CC -!- CATALYTIC ACTIVITY: 3-carboxy-2-hydroxy-4-methylpentanoate + NAD(+) = 3-carboxy-4-methyl-2-oxopentanoate + NADH.  
 CC -!- PATHWAY: Leucine biosynthesis; third step.  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- SIMILARITY: Belongs to the isocitrate and isopropylmalate dehydrogenases family. LeuB subfamily 1.

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 -----  
 EMBL; AF197452; AAC31390.1; -.  
 DR HSSP; P37412; 1CNZ.  
 DR HAMAP; MF\_01033; -.  
 DR InterPro; IPR001804; Iscdh.  
 DR InterPro; IPR004429; LeuB.  
 DR Pfam; PF00180; iscdh; 1.  
 DR TIGRFAMs; TIGR00169; leuB; 1.  
 DR PROSITE; PS00470; IDH\_IMDH; 1.  
 KW Oxidoreductase; Leucine biosynthesis; NAD; Plasmid.  
 SQ SEQUENCE 364 AA; 40542 MW; 0B94A8A092CE7FCD CRC64;

Query Match 31.7%; Score 44; DB 1; Length 364;  
 Best Local Similarity 47.4%; Pred. No. 36;

Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 7 CSLDGRSVLKTTGTTKDVV 25  
 DB 191 CSLDKSNVLKSSILWKEIV 209

RESULT 35  
 SCAG\_XENLA  
 ID SCAG\_XENLA STANDARD; PRT; 660 AA.  
 AC P51171;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Amiloride-sensitive sodium channel gamma-subunit (Epithelial Na+ channel gamma subunit) (Gamma ENAC) (Nonvoltage-gated sodium channel 1 gamma subunit) (SCNEG) (Gamma NACH).  
 DE Xenopus laevis (African clawed frog).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=83355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=93358264; PubMed=7631745;  
 RA Puoti A.; May A.; Canessa C.M.; Horisberger J.-D.; Schild L.; Rossier B.C.;  
 RT "The highly selective low-conductance epithelial Na channel of Xenopus laevis A6 kidney cells.";  
 RL Am. J. Physiol. 269:C188-C197 (1995).  
 CC -!- FUNCTION: Sodium permeable non-voltage-sensitive ion channel inhibited by the diuretic amiloride. Mediates the electrodiffusion of the luminal sodium (and water, which follows osmotically) through the apical membrane of epithelial cells. Controls the reabsorption of sodium in kidney, colon, lung and sweat glands. Also plays a role in taste perception.  
 CC -!- SUBUNIT: Heterotetramer of two alpha, one beta and one gamma subunit. A delta subunit can replace the alpha subunit (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- PTM: Phosphorylated on serine and threonine residues (By similarity).  
 CC -!- PTM: Ubiquitinated; this targets individual subunits for proteasome-mediated degradation (By similarity).  
 CC -!- SIMILARITY: Belongs to the amiloride-sensitive sodium channel family.

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 EMBL; U25342; AAA74972.1; -.  
 DR PIR; I51684; I51684.  
 DR InterPro; IPR004724; ENAC.  
 DR InterPro; IPR001873; Na-channel\_ASC.  
 DR Pfam; PF00858; ASC; 1.  
 DR PRINTS; PRO1078; AMINACHANNEL.  
 DR TIGRFAMs; TIGR00859; ENAC; 1.  
 DR PROSITE; PS01206; ASC; 1.  
 KW Ion transport; Sodium transport; Ionic channel; Transmembrane; Glycoprotein; Phosphorylation; Ubl conjugation; Sodium channel.  
 FT DOMAIN 1 55 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 56 76 POTENTIAL.  
 FT DOMAIN 77 545 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 546 566 POTENTIAL.  
 FT DOMAIN 567 660 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 149 149 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 213 213 N-LINKED (GLCNAC... ) (POTENTIAL).

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FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 498 498 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 660 AA; 75622 MW; 6735556DCE50B1C CRC64;

Query Match 31.7%; Score 44; DB 1; Length 660;
Best Local Similarity 50.0%; Pred. No. 70;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 PWTNCSLDGRSV 14
|...|:|:|:|
DB 371 PYSDCITMGDRDV 382

RESULT 36
ID DAB2 MOUSE STANDARD; PRT; 766 AA.
AC P98078; Q91W56; Q923E1;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
GN Disabled homolog 2 (DOC-2) (Mitogen-responsive phosphoprotein).
GN DAB2 OR DOC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

[1]
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=BAH/c; TISSUE=Macrophage;
RX MEDLINE=95294028; PubMed=7775479;
RA Xu X.-X., Yang W., Jackowski S., Rock C.O.;
RT "Cloning of a novel phosphoprotein regulated by colony-stimulating
RT factor 1 shares a domain with the Drosophila disabled gene product."
RL J. Biol. Chem. 270:14184-14191(1995).
RN [2]
SEQUENCE FROM N.A. (ISOFORM P96).
RP STRAIN=129/SV;
RC STRAIN=21261960; PubMed=11368898;
RX Sheng Z., Smith E.R., He J., Tuppen J.A., Martin W.D., Dong F.B.,
RA Xu X.-X.;
RT "Chromosomal location of murine disabled-2 gene and structural
RT comparison with its human ortholog."
RL Gene 268:31-39(2001).
RN [3]
SEQUENCE FROM N.A. (ISOFORM P67).
RP TISSUE=Kidney;
RC MEDLINE=23386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullah S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Component of the CSF-1 signal transduction pathway.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=p96;
CC IsoId=P98078-1; Sequence=Displayed;
CC Name=p93;

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IsoId=P98078-2; Sequence=VSP\_004182;  
 Name=p67;  
 IsoId=P98078-3; Sequence=VSP\_004183;  
 -!- DOMAIN: The PID domain specifically binds to the Aen-Pro-Xaa-Tyr(P) motif found in many tyrosine-phosphorylated proteins including growth factor receptors.  
 -!- PTM: Phosphorylated on serine residues in response to mitogenic growth-factor stimulation.  
 -!- SIMILARITY: Contains 1 PID domain.

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EMBL; U18869; AAB02646.1; -  
 EMBL; U18869; AAB02647.1; -  
 EMBL; U18869; AAB02645.1; -  
 EMBL; AF260580; AAG44669.1; -  
 EMBL; BC006588; AAH06588.1; -  
 EMBL; BC018887; AAH18887.1; -  
 MGD; MGI:109175; Dab2.

DR GO; GO:0005515; F-protein binding; IPI.  
 DR GO; GO:000904; P-cellular morphogenesis during differentiation; IMP.  
 DR GO; GO:0001701; P-embryonic development (sensu Mammalia); IMP.  
 DR GO; GO:0006898; P-receptor mediated endocytosis; IPI.  
 DR InterPro: IPR006020; PTB\_PID.  
 DR Pfam; PF00640; PID; 1.  
 DR SMART; SM00462; PTE; 1.  
 DR PROSITE; PS01179; PID; 1.  
 KW Alternative splicing; Phosphorylation.  
 FT DOMAIN 45 196  
 FT VARSPLIC 209 229  
 FT Missing (in isoform p93).  
 FT /FTID=VSP\_004182.  
 FT VARSPLIC 230 447  
 FT Missing (in isoform p67).  
 FT /FTID=VSP\_004183.  
 FT CONFLICT 10 10 T -> A (IN REF. 3; AAH06588).  
 FT CONFLICT 224 224 D -> G (IN REF. 3; AAH06588).  
 FT CONFLICT 338 338 V -> G (IN REF. 2).  
 FT CONFLICT 454 454 P -> L (IN REF. 3).  
 FT CONFLICT 490 490 P -> A (IN REF. 3).  
 FT CONFLICT 536 536 R -> G (IN REF. 3).  
 FT CONFLICT 553 553 S -> P (IN REF. 3; AAH06588).  
 SQ SEQUENCE 766 AA; 82363 MW; 1F3EFD6DC84B100 CRC64;

Query Match 31.7%; Score 44; DB 1; Length 766;  
 Best Local Similarity 41.7%; Pred. No. 83;  
 Matches 10; Conservative 3; Mismatches 9; Indels 2; Gaps 1;

QY 2 PWTNCSLDGRSVL--KGTTEKD 23  
 |...|:|:|:|  
 DB 92 RIWNAISLGKIIDEKTVIEHE 115

RESULT 37  
 ID DAB2 RAT STANDARD; PRT; 768 AA.  
 AC O88797; O55049; O55050; O55051; O88798;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Disabled homolog 2 (DOC-2) (Mitogen-responsive phosphoprotein) (C9).  
 GN DAB2 OR DOC2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
 RC STRAIN=Sprague-Dawley; TISSUE=Prostate;

RX MEDLINE=98344831; PubMed=9681506;  
RA Tseung C.-P., Ely B.D., Li Y., Pong R.-C., Hsieh J.-T.;  
RT "Regulation of rat DOC-2 gene during castration-induced rat ventral  
RT prostate degeneration and its growth inhibitory function in human  
RT prostatic carcinoma cells.";  
RL Endocrinology 139:3542-3553(1998).  
[2]  
RP SEQUENCE OF 2-47; 117-189; 634-687 AND 753-768 FROM N.A.  
RP TISSUE=Kidney, and Prostate;  
RA Lau K.M., Mok S.C., Ho S.M.;  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Component of the CSP-1 signal transduction pathway (By  
CC similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=sp2;  
CC IsoId=C88797-1; Sequence=Displayed;  
CC Name=sp59;  
CC IsoId=C88797-2; Sequence=VSP\_004184;  
CC -!- TISSUE SPECIFICITY: Prostate;  
CC -!- DOMAIN: The PID domain specifically binds to the An-Pro-Xaa-  
CC Tyr(P) motif found in many tyrosine-phosphorylated proteins  
CC including growth factor receptors.  
CC -!- PPM: Phosphorylated.  
CC -!- SIMILARITY: Contains 1 PID domain.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; U95177; AAC33405.1; -;  
DR EMBL; U95178; AAC33406.1; -;  
DR EMBL; AF045657; AAC03360.1; -;  
DR EMBL; AF045658; AAC03361.1; -;  
DR EMBL; AF045659; AAC03362.1; -;  
DR EMBL; AF045660; AAC03363.1; -;  
DR InterPro; IPR005020; PTB\_PID.  
DR Pfam; PF00640; PID; 1.  
DR SMART; SM00462; PTB; 1.  
DR PROSITE; PS01179; PID; 1.  
KW Alternative splicing; Phosphorylation.  
FT DOMAIN 45 196  
FT VARSPLIC 230 447  
FT CONFLICT 3 4  
FT CONFLICT 186 186 N -> TN (IN REF. 2).  
FT CONFLICT 675 675 S -> P (IN REF. 2).  
FT CONFLICT 764 768 GNPPA -> WKSFC (IN REF. 2).  
SQ SEQUENCE 768 AA; 82376 MW; 930FB25248ADAC6E CRC64;  
  
Query Match 31.7%; Score 44; DB 1; Length 768;  
Best Local Similarity 41.7%; Pred. No. 83;  
Matches 10; Conservative 3; Mismatches 9; Indels 2; Gaps 1;  
  
Qy 2 RPTWNCSLDGRSVL-KTGTTEKD 23  
Db 92 RIWNISLGIKIDKGTGVEH 115  
  
RESULT 38  
DAB2 HUMAN  
ID DAB2 HUMAN STANDARD; PRT; 770 AA.  
AC P98052; Q13598; Q9BTY0; Q9UK04;  
DT 01-FEB-1996 (Rel. 33, Created)  
DI 01-OCT-1996 (Rel. 34, Last sequence update)  
DE 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Disabled homolog 2 (Differentially expressed protein 2) (DOC-2).  
GN DAB2 OR DOC2.  
OS Homo sapiens (Human).

OC BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC [1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=96301397; PubMed=8660969;  
RA Albertsen H.M., Smith S.A., Melis R., Williams B., Holik P.,  
RA Stevens J., White R.;  
RT "Sequence, genomic structure, and chromosomal assignment of human  
RT DOC-2.";  
RL Genomics 33:207-213(1996).  
[2]  
RN SEQUENCE FROM N.A.  
RA Sheng Z., He J., Sun W., Smith E.R., Fazili Z., Feng D.B., Xu X.;  
RT "Gene structure, sequence, and promoter of human disabled-2.";  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
[3]  
RN SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
RX MEDLINE=99270207; PubMed=10340382;  
RA Fazili Z., Sun W., Mittelstaedt S., Cohen C., Xu X.-X.;  
RT "Disabled-2 inactivation is an early step in ovarian tumorigenicity.";  
RL Oncogene 18:3103-3113(1999).  
[4]  
RN SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND ALTERNATIVE SPLICING.  
RC TISSUE=Ovary;  
RX MEDLINE=98281865; PubMed=9620555;  
RA Mok S.C., Chan W.Y., Wong K.-K., Cheung K.K., Lau C.C., Ng S.W.,  
RA Baldini A., Colitti C.V., Rock C.O., Berkowitz R.S.;  
RT "DOC-2, a candidate tumor suppressor gene in human epithelial ovarian  
RT cancer.";  
RL Oncogene 16:2381-2387(1998).  
[5]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.N., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Fallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[6]  
RN SEQUENCE OF 44-304 FROM N.A.  
RC TISSUE=Ovary;  
RX MEDLINE=94148289; PubMed=8314147;  
RA Mok S.C., Wong K.-K., Chan R.K.W., Lau C.C., Tsao S.-W., Knapp R.C.,  
RA Berkowitz R.S.;  
RT "Molecular cloning of differentially expressed genes in human  
RT epithelial ovarian cancer.";  
RL Gynecol. Oncol. 52:247-252(1994).  
CC -!- FUNCTION: Component of the CSP-1 signal transduction pathway (By  
CC similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=P98082-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=P98082-2; Sequence=VSP\_004181;  
CC -!- TISSUE SPECIFICITY: Expressed in deep invaginations, inclusion

CC cysts and the surface epithelial cells of the ovary. Also  
 CC expressed in breast epithelial cells, spleen, thymus, prostate,  
 CC testis, macrophages, fibroblasts, lung epithelial cells, placenta,  
 CC brain stem, heart and small intestine.  
 CC -!- PTM: Phosphorylated (By similarity).  
 CC -!- SIMILARITY: Contains 1 PID domain.  
 CC -----  
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 CC -----  
 CC EMBL; U39050; AAC50824.1; -  
 CC EMBL; U41111; AAB19032.1; -  
 CC EMBL; AF205890; AAF2161.1; -  
 CC EMBL; AF188298; AAF05540.1; -  
 CC EMBL; U53446; AAA98975.1; -  
 CC EMBL; BC003064; AAH03064.1; -  
 CC EMBL; L16896; AAA93195.1; -  
 CC PIR; G02228; G02228  
 CC Genew; HGNC:2662; DAB2.  
 CC MIM; 601236; -  
 CC GO; GO:0008283; P:cell proliferation; TAS.  
 CC InterPro; IPR006020; PTB\_PID.  
 CC Pfam; PF00640; PID; 1.  
 CC SMART; SM00462; PTB; 1.  
 CC PROSITE; PS01179; PID; 1.  
 CC Alternatve splicing; Phosphorylation.  
 KW DOMAIN 45 196  
 FT VARSPLIC 230 447  
 FT MISSING (in isoform 2).  
 FT /FTID=VSP\_004181.  
 FT CONFLICT 44 47 KGDG -> PRVC (IN REF. 6).  
 FT CONFLICT 82 82 R -> A (IN REF. 3 AND 5).  
 FT CONFLICT 148 148 A -> T (IN REF. 4).  
 FT CONFLICT 197 197 M -> R (IN REF. 4).  
 FT CONFLICT 209 229 MISSING (IN REF. 3).  
 FT CONFLICT 230 232 ESK -> VCF (IN REF. 3 AND 6).  
 FT CONFLICT 275 275 S -> L (IN REF. 3, 4 AND 5).  
 FT CONFLICT 302 304 QPD -> HTR (IN REF. 6).  
 FT CONFLICT 498 498 L -> Q (IN REF. 3).  
 FT CONFLICT 770 770 AA; 82506 MW; 317F3F1343AFAP CRC64;  
 Query Match 31.7%; Score 44; DB 1; Length 770;  
 Best Local Similarity 41.7%; Pred. No. 83;  
 Matches 10; Conservative 3; Mismatches 9; Indels 2; Gaps 1;  
 RESULT 39  
 YU30\_RALSO  
 ID YU30\_RALSO STANDARD; PRT; 1582 AA.  
 AC Q8XV02;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hypothetical UPF0192 protein RSC3030 precursor.  
 GN RSC3030 OR RS04727.  
 OS Ralstonia solanacearum (Pseudomonas solanacearum)  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Burkholderiaceae; Ralstonia.  
 CC NCBI\_TaxID=305;  
 CC [1]  
 RC STRAIN=GMT N.A.  
 RC MEDLINE=21681879; PubMed=11823852;  
 RX Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,  
 RA Ariat M., Billault A., Brottier P., Camus J.C., Catolico L.,

RA Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,  
 RA Gaspin C., Laveie M., Moisan A., Robert C., Saurin W., Schiex T.,  
 RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,  
 RA Weissenbach J., Boucher C.A.;  
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum";  
 RL Nature 415:497-502(2002).  
 CC -!- SIMILARITY: Belongs to the UPF0192 family.  
 CC -----  
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 CC -----  
 CC EMBL; AL646073; CAD16739.1; -  
 CC InterPro; IPR008930; Terp\_cyc\_toroid.  
 KW Hypothetical protein; Signal; Complete proteome.  
 FT SIGNAL 1 15 POTENTIAL.  
 FT CHAIN 16 1582 HYPOTHETICAL PROTEIN RSC3030.  
 FT SEQUENCE 1582 AA; 170090 MW; 8683D148F5AE3C2A CRC64;  
 Query Match 31.7%; Score 44; DB 1; Length 1582;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+02;  
 Matches 10; Conservative 2; Mismatches 4; Indels 4; Gaps 1;  
 QY 4 WTNCSDLGRSVLKTGTTEKD 23  
 Db 278 WT----DGVGLASGITQAD 293  
 RESULT 40  
 YHGH\_ECOLI  
 ID YHGH\_ECOLI STANDARD; PRT; 227 AA.  
 AC P46846;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical protein yhgh.  
 GN YHGH OR B3413.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 CC NCBI\_TaxID=562;  
 CC [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RC MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12";  
 RL Science 277:1453-1474(1997).  
 CC -!- SIMILARITY: TO H.INFLUENZAE COMF AND B.SUBTILIS COMFC.  
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 CC -----  
 CC EMBL; U18997; AAA58211.1; ALT\_INIT.  
 CC EMBL; AE000417; AAC76438.1; ALT\_INIT.  
 CC EcoGene; EG12934; yhgH.  
 CC InterPro; IPR005222; ComF.  
 CC InterPro; IPR000836; PRTtransferase.  
 CC Pfam; PF00156; Pribosyltran; 1.  
 CC TIGRFAMs; TIGR00201; comF; 1.  
 KW Hypothetical protein; Complete proteome.



FT DOWAIN 8 54 CYS-RICH.  
SQ SEQUENCE 227 AA; 25726 MW; BA8768610CDA03BE CRC64;  
Query Match 31.3%; Score 43.5; DB 1; Length 227;  
Best Local Similarity 34.8%; Pred.No.26;  
Matches 8; Conservative 4; Mismatches 8; Indels 3; Gaps 1;  
QY 1 CRP---WTNGSLDGRSVLKTGTT 20  
Db 138 CQPLSRWLHCQNDSEAVTRTRAT 160

Search completed: May 5, 2004, 14:38:41  
Job time : 1.96918 secs

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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:34:21 ; Search time 8.56164 Seconds

(without alignments)  
921.313 Million cell updates/sec

Title: US-10-067-122b-2\_COPY\_133\_157

Perfect score: 139

Sequence: 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_25:

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	211	11	Q8R037
2	75	54.0	267	6	Q02764
3	66	47.5	274	6	Q7YRL5
4	65	46.8	278	6	Q8SQ34
5	63	45.3	223	4	Q86YX5
6	62	44.6	289	11	Q8K2X6
7	57	41.0	277	6	Q8WMQ2
8	57	41.0	483	13	Q800K7
9	54.5	39.2	196	11	Q8VC17
10	54.5	39.2	232	16	Q88PW0
11	54.5	39.2	275	11	Q80WM9
12	53.5	38.5	772	17	Q9UYF4
13	51	36.7	138	10	Q7XBZ5
14	51	36.7	191	10	Q8S7E9
15	51	36.7	276	13	Q9DDD2
16	51	36.7	810	5	O61228

#### ALIGNMENTS

##### RESULT 1

Q8R037 PRELIMINARY; PRT; 211 AA.  
ID Q8R037  
AC Q8R037;  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Similar to tumor necrosis factor receptor superfamily, member 9.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=uterus;  
RA Strausberg R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC028507; AAH28507.1; -  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 1.  
DR SMART; SM00208; TNFR; 2.  
DR PROSITE; PS01186; EGF 2; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
KW Receptor.  
SQ SEQUENCE 211 AA; 22452 MW; 1EECA84EA32A8D50 CRC64;

Query Match 100.0%; Score 139; DB 11; Length 211;

Best Local Similarity 100.0%; Pred. No. 6.8e-14;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25

Db 133 CRPWTNCSLDGRSVLKTGTTEKDVV 157

##### RESULT 2

O02764

```

ID O02764 PRELIMINARY; PRT; 267 AA.
AC O02764;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE OX40 precursor (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA West K.A., Li A.W., Rowden G.;
RC STRAIN=Chbb:HM;
RT "Expression of OX40 and OX40 ligand genes in rabbit HTLV-I-transformed
T cell lines.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003911; BAA20059.1; -
DR HSSP; Q92956; LJMA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00650; TNFR_NGFR_2; 2.
KW Signal.
FT NON TER 1 1
FT SIGNAL <1 18 POTENTIAL.
FT CHAIN 19 267 OX40.
FT SEQUENCE 267 AA; 28489 MW; A8B4CD3173C9500B CRC64;

Query Match 54.0%; Score 75; DB 6; Length 267;
Best Local Similarity 48.0%; Pred. No. 0.0015;
Matches 12; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 135 CRPWTNCTLAGKRTLPASSISDAV 159

RESULT 3
QYRL5 PRELIMINARY; PRT; 274 AA.
AC QYRL5;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CD40.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang S., Sim G.-K.;
RT "Canine CD40 and CD40 Ligand cDNA Sequences.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY333789; AAP86653.1; -
DR SEQUENCE 274 AA; 30284 MW; 9723789A07FAB6DB CRC64;

Query Match 47.5%; Score 66; DB 6; Length 274;
Best Local Similarity 40.0%; Pred. No. 0.041;
Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 161 CRPWTSCETKGLVQVAGNKTVDI 185

RESULT 4
Q8SQ34 PRELIMINARY; PRT; 278 AA.
ID -Q8SQ34

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AC Q8SQ34;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE CD40.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA West K.A., Li A.W., Rowden G.;
RT "Characterization of the Porcine CD40 Molecule.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF248545; AAL92924.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001388; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00650; TNFR_NGFR_2; 4.
DR SEQUENCE 278 AA; 30951 MW; 20D446B44AF93DD2 CRC64;

Query Match 46.8%; Score 65; DB 6; Length 278;
Best Local Similarity 44.0%; Pred. No. 0.061;
Matches 11; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25
Db 161 CQPWTSCEKGLVQVAGNKTVDV 185

RESULT 5
Q86YK5 PRELIMINARY; PRT; 223 AA.
ID Q86YK5
AC Q86YK5;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 (Fragment).
GN TNFRSF5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA He X., Xu L., Zeng Y.;
RT "Transcripts of CD40 isoform in peripheral mononuclear cells.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY225405; AAO43990.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0004888; F:binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001993; Mitoch carrier.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF_2; 1.

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DR PROSITE; PS00215; MITOCH CARRIER; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_2; 4.  
KW Receptor.  
FT NON TER 223 223  
SQ SEQUENCE 223 AA; 24659 MW; 85C63C20BC4E0B1C CRC64;

Query Match 45.38; Score 63; DB 4; Length 223;  
Best Local Similarity 44.08; Pred. No. 0.999;  
Matches 11; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
| | | | | : : : : :  
Db 161 CPEWTSCEKDLVVOQAGTNTKTDV 185

RESULT 6  
Q8K2X6 PRELIMINARY; PRT; 289 AA.  
AC Q8K2X6;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Similar to tumor necrosis factor receptor superfamily, member 5.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC029254; AAH29254.1; .  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0005840; C:ribosome; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
DR GO; GO:0006915; P:apoptosis; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR GO; GO:006412; P:protein biosynthesis; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR008063; F:receptor.  
DR InterPro; IPR01005; Myb DNA binding.  
DR InterPro; IPR01865; Ribosomal\_S2.  
DR InterPro; IPR01368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR PRINTS; PR01680; FASRECEPTOR.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS00037; MYB\_1; 1.  
DR PROSITE; PS00962; RIBOSOMAL\_S2\_1; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_2; 4.  
KW Receptor.  
SQ SEQUENCE 289 AA; 32077 MW; DBE93B1E439F1E2A CRC64;

Query Match 44.68; Score 62; DB 11; Length 289;  
Best Local Similarity 40.08; Pred. No. 0.19;  
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
| | | | | : : : : :  
Db 161 CPEWTSCEKDLVVOQAGTNTKTDV 185

RESULT 7  
Q8WMQ2 PRELIMINARY; PRT; 277 AA.  
AC Q8WMQ2;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Membrane protein CD40 (Fragment).  
OS Evis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zawitkowski M.S.; Russ G.R.; Krishnan R.;  
RT "Cloning and expression of the ovine CD40 molecule and the inhibition of the mixed lymphocyte reaction by the ovine CD40-EGFP fusion protein."  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AV072798; AAL68402.1; .  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
DR GO; GO:0006915; P:apoptosis; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR008063; Fas receptor.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR PRINTS; PR01680; FASRECEPTOR.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_2; 1.  
FT NON TER 277 277  
SQ SEQUENCE 277 AA; 30465 MW; 619F28BEA18A0D29 CRC64;

Query Match 41.08; Score 57; DB 6; Length 277;  
Best Local Similarity 40.08; Pred. No. 1.1;  
Matches 10; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDVV 25  
| | | | | : : : : :  
Db 161 CPEWTSCEKDLVVOQAGTNTKTDV 185

RESULT 8  
Q800K7 PRELIMINARY; PRT; 483 AA.  
AC Q800K7;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Tumor necrosis factor receptor-2.  
GN TNFR-2.  
OS Paralichthys olivaceus (Flounder).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
OC Pleuronectoidae; Paralichthyidae; Paralichthys.  
OX NCBI\_TaxID=8255;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Park C.; Kurobe T.; Hirono I.; Aoki T.;  
RT "Cloning and characterization of cDNAs for two distinct tumor necrosis factor receptor superfamily genes from Japanese flounder Paralichthys olivaceus."  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB080947; BAC65226.1; .  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_2; 3.  
KW Receptor.  
SQ SEQUENCE 483 AA; 52227 MW; EE55874A8C7F2085 CRC64;

Query Match 41.08; Score 57; DB 13; Length 483;  
Best Local Similarity 44.08; Pred. No. 2.1;  
Matches 11; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

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QY 1 CRPWTNCSLDGRSVLKTGTTEKDV 25
DB 168 CRPFTDC--HGKAVVRKGNITSDTV 190

RESULT 9
Q8VCL17 PRELIMINARY; PRT; 196 AA.
AC Q8VCL17
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022125; AAH22125.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; FAS_receptor.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR_2; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 196 AA; 21555 MW; 2A33FF8905E260E8 CRC64;

Query Match 39.2%; Score 54.5; DB 11; Length 196;
Best Local Similarity 47.8%; Pred. No. 2;
Matches 11; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 CRPWTNCSLDGRSVLKTGTTEKD 23
DB 99 CLPWTNCSAFOQEV-RRGTNSTD 120

RESULT 10
Q8BPW0 PRELIMINARY; PRT; 232 AA.
AC Q8BPW0;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Conserved domain protein.
GN PP0738.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzes A.,
RA Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
RA Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuenmiller B.,
RA Fraser C.M.;

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RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AF016776; AAN66363.1; -.
DR TIGR; PF0738; -.
KW Complete proteome.
SQ SEQUENCE 232 AA; 25566 MW; A16A03C40B1EC8F0 CRC64;

Query Match 39.2%; Score 54.5; DB 16; Length 232;
Best Local Similarity 57.1%; Pred. No. 2.4;
Matches 12; Conservative 2; Mismatches 4; Indels 3; Gaps 2;

QY 1 CRPWTNCSLDGRSVLKTGTTE 21
DB 73 CHAW--CSLDG-LILNTGTTD 90

RESULT 11
Q80WM9 PRELIMINARY; PRT; 275 AA.
AC Q80WM9;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 14 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Thymus;
RA Benencia F., Conejo-Garcia J.R., Courreges M.C., Coukos G.;
RT "Light regulation in a murine model of ovarian carcinoma.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY264405; AAO89081.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; FAS_receptor.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR_4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor; Signal.
FT SIGNAL 1 38 Potential.
SQ SEQUENCE 275 AA; 30171 MW; C4A7EAD8EFC0521D CRC64;

Query Match 39.2%; Score 54.5; DB 11; Length 275;
Best Local Similarity 47.8%; Pred. No. 2.9;
Matches 11; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 CRPWTNCSLDGRSVLKTGTTEKD 23
DB 179 CLPWTNCSAFOQEV-RRGTNSTD 200

RESULT 12
Q9JVF4 PRELIMINARY; PRT; 772 AA.
AC Q9JVF4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Chemotaxis histidine kinase (CHEA).
GN PYRAB15540 OR PAB1332.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.

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OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GS / Orsay;
RA Hellig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ248288; CAB50458.1; -
DR PIR: D75002; D75002.
DR HSP: Q56310; I33Q.
DR GO: GO:0005737; C:cytoplasm; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0016301; F:kinase activity; IEA.
DR GO: GO:0001555; F:two-component sensor molecule activity; IEA.
DR GO: GO:0006935; P:chemotaxis; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR004358; Bact_sens_pr_C.
DR InterPro: IPR002545; CHEW.
DR InterPro: IPR004105; H-kinase dim.
DR InterPro: IPR005467; His_kinase.
DR InterPro: IPR008207; Hpt_N.
DR InterPro: IPR008208; Hpt_N.
DR Pfam: PF01584; Chew; 1.
DR Pfam: PF02895; H-kinase dim; 1.
DR Pfam: PF02518; HATPase_C; 1.
DR Pfam: PF01627; Hpt; 1.
DR PRINTS: PR00344; BCTRLSENSOR.
DR ProDom: PD003142; Hpt_N; 1.
DR SMART: SM00360; Chew; 1.
DR SMART: SM00387; HATPase_C; 1.
DR SMART: SM00073; HPT; 1.
DR PROSITE: PS00851; CHEW; 1.
DR PROSITE: PS50109; HIS_KIN; 1.
DR PROSITE: PS50894; HPT; 1.
KW Kinase. Complete proteome.
SQ SEQUENCE 772 AA; 86113 MW; 314766ACAD2108B CRC64;

Query Match 38.5%; Score 53.5; DB 17; Length 772;
Best Local Similarity 45.5%; Pred. No. 13;
Matches 10; Conservative 5; Mismatches 4; Indels 3; Gaps 1;

OY 4 WTNCSLDGRSVLKTGTTEKDVV 25
Db 207 WTN---PGRDVIESGNLDKQVI 225

RESULT 13
OYXBZ5 PRELIMINARY; PRT; 138 AA.
AC OYXBZ5
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OSJNBA0057L21.8
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
CX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice
RT chromosome 10.";
RL Science 300:1566-1569(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
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RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE017121; AAP55081.1; -
KW Hypothetical protein.
SQ SEQUENCE 138 AA; 15173 MW; 0627C2D8842A1757 CRC64;

Query Match 36.7%; Score 51; DB 10; Length 138;
Best Local Similarity 66.7%; Pred. No. 4.8;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 CRPWTNCSLDGR 12
Db 78 CRPWELCSVDPR 89

RESULT 14
OY87E9 PRELIMINARY; PRT; 191 AA.
AC OY87E9
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN OSJNBA0057L21.8
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
CX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pal G.,
RA VanKen S.B., Utterback T.R., Feidblyum T.V., Kalb E., Quackenbush J.,
RA Salzberg S.L., White O., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNBA0057L21 genomic sequence.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC087595; AAL7907.1; -
DR Gramene; Q87B9; -
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 191 AA; 20559 MW; C4C856D83BC4E14B CRC64;

Query Match 36.7%; Score 51; DB 10; Length 191;
Best Local Similarity 66.7%; Pred. No. 6.9;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 CRPWTNCSLDGR 12
Db 131 CRPWELCSVDPR 142

RESULT 15
OY87E9 PRELIMINARY; PRT; 276 AA.
AC OY87E9
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Human CD40-homologue.
GN TNFSF5.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Tregaskes C.A.;
RT Thesis (2001); University of Reading, Reading, UNITED KINGDOM.
DR EMBL: AJ293700; CAC20218.1; -
DR HSP: Q92956; IJMA.
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DR GO:0016020; C:membrane; IEA.
DR GO:0005634; C:nucleus; IEA.
DR GO:0003677; P:DNA binding; IEA.
DR GO:0004888; P:transmembrane receptor activity; IEA.
DR GO:0006915; P:apoptosis; IEA.
DR GO:0006955; P:immune response; IEA.
DR GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR008063; Fas receptor.
DR InterPro: IPR001005; Myb DNA binding.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6_3.
DR PRINTS: PR01680; FASRECEPTOR.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00037; MYB_1; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS00500; TNFR_NGFR_2; 3.
SQ SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454E CRC64;

Query Match 36.7%; Score 51; DB 13; Length 276;
Best Local Similarity 40.0%; Pred. No. 10;
Matches 10; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKLTGTTEKDV 25
DB 162 CHFWTSCBEKGLVVKVKGNTSDVI 186

RESULT 16
O61228 PRELIMINARY; PRT; 810 AA.
AC O61228;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Thr4 protein.
GN THRA.
OS Tenbrio molitor (Yellow mealworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Tenebrionidae; Tenebrio.
OX NCBI_TaxID=7067;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99449601; PubMed=10518792;
RA Mouillet J.F., Bousquet F., Sedano N., Alabouvette J., Nicolai M.,
RA Zelus D., Laudet V., Delachambre J.,
RT "Cloning and characterization of new orphan nuclear receptors and
RT their developmental profiles during Tenebrio metamorphosis.";
RL Eur. J. Biochem. 265:972-981(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
DR EMBL: AJ005685; CAA06670.1; -.
DR HSP; P19793; 2NLL.
DR GO:0005634; C:nucleus; IEA.
DR GO:0003707; P:steroid hormone receptor activity; IEA.
DR GO:0003700; P:transcription factor activity; IEA.
DR GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO:0006350; P:transcription; IEA.
DR InterPro: IPR000536; Hormone rec lig.
DR InterPro: IPR001723; Steroid_receptor.
DR InterPro: IPR008946; Steroid_receptor.
DR InterPro: IPR001628; Znf_C4steroid.
DR Pfam: PF00104; hormone_rec; 1.
DR Pfam: PF00105; zf-C4; 1.
DR PRINTS: PR00398; STRDHORMONER.
DR PRINTS: PR00047; STROIDFINGER.
DR ProDom: PD000035; Znf_C4steroid; 1.
DR SMART: SM00430; HOL1_1.
DR SMART: SM00399; Znf_C4; 1.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 810 AA; 89535 MW; A55D987DCFC7F489 CRC64;

Query Match 36.7%; Score 51; DB 2; Length 3025;
Best Local Similarity 54.5%; Pred. No. 1.5e+02;
Matches 12; Conservative 2; Mismatches 6; Indels 2; Gaps 2;

QY 3 PWTNCSLDGRSVLK-TGTEKD 23
DB 2110 PWT-CHADGRVLAEPGTGASED 2130

RESULT 18
Q9M2A5 PRELIMINARY; PRT; 230 AA.
ID Q9M2A5;
AC Q9M2A5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
SQ SEQUENCE 3025 AA; 312521 MW; 6F4BC965DAB19F25 CRC64;

Query Match 36.7%; Score 51; DB 2; Length 3025;
Best Local Similarity 54.5%; Pred. No. 1.5e+02;
Matches 12; Conservative 2; Mismatches 6; Indels 2; Gaps 2;

QY 3 PWTNCSLDGRSVLK-TGTEKD 23
DB 2110 PWT-CHADGRVLAEPGTGASED 2130

RESULT 18
Q9M2A5 PRELIMINARY; PRT; 230 AA.
ID Q9M2A5;
AC Q9M2A5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
SQ SEQUENCE 3025 AA; 312521 MW; 6F4BC965DAB19F25 CRC64;
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01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
Hypothetical protein.  
F15G16.120.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eursids II; Brassicales; Brassicaceae; Arabidopsis.  
NCBI\_taxid=3702;  
[1]  
SEQUENCE FROM N.A.  
RP De Haan M., Maarse A.C., Grivell L.A., Mewes H.W., Lemcke K.,  
RA Mayer K.F.X., Quetier F., Salanoubat M.;  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
[2]  
SEQUENCE FROM N.A.  
RP EU Arabidopsis sequencing project;  
RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RL EMBL; ALI32959; CAB71103.1; -.  
DR PIR; T47965; T47965.  
KW Hypothetical protein.  
SQ SEQUENCE 354 AA; 39750 MW; 3BC6D1190885CF8C CRC64;  
Query Match 36.0%; Score 50; DB 10; Length 354;  
Best Local Similarity 52.4%; Pred. NO. 20;  
Matches 11; Conservative 3; Mismatches 5; Indels 2; Gaps 1;  
QY 4 WTNCSS-LDGRSVLKTGTTEK 22  
DD 93 WTVISRFDLGKSLVKGATNK 113  
RESULT 21  
Q82WA1 PRELIMINARY; PRT; 363 AA.  
ID Q82WA1  
AC Q82WA1;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Riboflavin biosynthesis bifunctional RibD (EC 3.5.4.26).  
RN RIBD OR NE0793.  
OS Nitrosomonas europaea.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;  
OC Nitrosomonadaceae; Nitrosomonas.  
NCBI\_TaxID=915;  
[1]  
SEQUENCE FROM N.A.  
RP STRAIN=ATCC 19718 / IF0 14298;  
RX MEDLINE=22586410; PubMed=12700255;  
RA Chain P., Imerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,  
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Savavedra-Soto L.A.,  
RA Arciero D.M., Hommes N.G., Whitaker M.M., Arp D.J.;  
RA "Complete genome sequence of the ammonia-oxidizing bacterium and  
RT obligate chemolithoautotroph Nitrosomonas europaea";  
RJ J. Bacteriol. 185:2759-2773 (2003).  
DR EMBL: BX321858; CAD84704.1; -.  
DR GO; GO:0008703; F:5-amino-6-(5-phosphoribosylamino)uracil red. .; IEA.  
DR GO; GO:0008935; F:diadenosine diphosphate; ribosylaminopyrimidine. .; IEA.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR GO; GO:0009231; P:vitamin B2 biosynthesis; IEA.  
DR InterPro; IPR002125; GCMF/cyt deam.  
DR InterPro; IPR004794; Eubact\_RibD.  
DR InterPro; IPR002734; RibD\_C.  
DR Pfam; PF00363; GCMF\_cyt deam; 1.  
DR Pfam; PF01872; RibD\_C; 1.  
DR TIGRFAMS; TIGR00326; eubact\_ribd; 1.  
DR TIGRFAMS; TIGR00227; ribD\_Cterm; 1.  
DR PROSITE; PS00903; CYT\_DCMF\_DEAMINASES; 1.  
KW Hydrolase; Complete proteome.  
SQ SEQUENCE 363 AA; 39834 MW; 38E50089EA2276BB CRC64;  
Query Match 36.0%; Score 50; DB 16; Length 363;  
Best Local Similarity 41.7%; Pred. NO. 20;

Matches 10; Conservative 3; Mismatches 7; Indels 4; Gaps 1;

QY 2 RPWTN-----CSLDGRSVLKTGTTE 21  
 |||||:|||||:  
 Db 149 RPWRTKIAASFDGRALKNGKSQ 172

## RESULT 22

Q7VQA7  
 ID Q7VQA7 PRELIMINARY; PRT; 378 AA.  
 AC Q7VQA7;  
 DT 01-OCT-2003 (TREMELrel. 25, Created)  
 DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE Bifunctional pyrimidine deaminase/reductase in pathway of riboflavin  
 synthesis (EC 3.5.4.26) (EC 1.1.1.193).  
 GN RIBD OR BFL234.  
 OS Candidatus Blochmannia floridanus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.  
 OX NCBI\_TaxID=203907;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22784745; PubMed=12886019;  
 RA Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candelas F.,  
 RA Latorre A., Rausell C., Kamerbeek J., Gadau J., Hoellidobler B.,  
 RA van Ham R.C.H.J., Gross R., Moya A.;  
 RT "The genome sequence of Blochmannia floridanus: comparative analysis  
 of reduced genomes";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393(2003).  
 DR EMBL; BX248584; CAD33747.1; -;  
 KW Hydroxylase; Oxidoreductase; Complete proteome.  
 SQ SEQUENCE 378 AA; 42508 MW; 21ACBD8EF4FF8779 CRC64;

Query Match 36.0%; Score 50; DB 16; Length 378;  
 Best Local Similarity 43.5%; Pred. No. 21;  
 Matches 10; Conservative 4; Mismatches 5; Indels 4; Gaps 1;

QY 3 PWTN-----CSLDGRSVLKTGTTE 21  
 |||||:|||||:  
 Db 154 PWIKVKLAASLDGRTAMTKGSK 176

## RESULT 23

Q9SX68  
 ID Q9SX68 PRELIMINARY; PRT; 170 AA.  
 AC Q9SX68;  
 DT 01-MAY-2000 (TREMELrel. 13, Created)  
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)  
 DE FL1A17.10 protein (Putative ribosomal protein).  
 GN FL1A17.10.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ecv. Columbia;  
 RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,  
 RA Lee J.M., Li J., Gonzalez A., Liu A., Liu K., Vaysberg M., Sakano H.,  
 RA Chin C., Choi E., Chou J., Altafi H., Araujo R., Brooks S.,  
 RA Bushler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,  
 RA Hwang B., Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P.,  
 RA Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;  
 RT "Arabidopsis thaliana chromosome I BAC FL1A17 sequence";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 [2]

SEQUENCE FROM N.A.  
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Barh J., Chung M.K.,  
 RA Goldsmith A.D., Lee J.M., Toriumi M., Yu G., Brooks S., Chao Q.,  
 RA Chen H., Karlin-Neumann G., Kim C., Lam B., Miranda M., Nguyen M.,

RA Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,  
 RA Theologis A.;  
 RT "Full Length cDNA of gene FL1A17.10 (GI:5733872).";  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC007932; AAD49760.1; -;  
 DR EMBL; AF336922; AAG54003.1; -;  
 DR PIR; E96523; E96523.

DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0005840; C:ribosome; IEA.  
 DR GO; GO:0003735; F:protein biosynthesis; IEA.  
 DR GO; GO:0006412; P:protein biosynthesis; IEA.  
 DR InterPro; IPR004389; Ribosomal\_L18bac.  
 DR InterPro; IPR005484; Ribosomal\_L18p.  
 DR Pfam; PF00861; Ribosomal\_L18p; 1.  
 DR ProDom; PD001394; Ribosomal\_L18bac; 1.  
 DR TIGRFAMs; TIGR00060; L18\_bact; 1.  
 KW Ribosomal protein.  
 SQ SEQUENCE 170 AA; 18726 MW; 841F1EF9B11D1BB4 CRC64;

Query Match 35.6%; Score 49.5; DB 10; Length 170;  
 Best Local Similarity 40.0%; Pred. No. 11;  
 Matches 10; Conservative 7; Mismatches 5; Indels 3; Gaps 1;

QY 2 RPWTNCSLDGRSVL---KTGTTEKD 23  
 :|||:|||||:  
 Db 32 KPWSRSSLSQSRSMVVEAKTKSSD 56

## RESULT 24

Q8RS35  
 ID Q8RS35 PRELIMINARY; PRT; 360 AA.  
 AC Q8RS35;  
 DT 01-JUN-2002 (TREMELrel. 21, Created)  
 DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE Deaminase.  
 GN TOXE.  
 OS Pseudomonas glumae.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Burkholderiaceae; Burkholderia.  
 OX NCBI\_TaxID=337;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MAFF327195;  
 RA Suzuki F.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [2]

SEQUENCE FROM N.A.  
 RC STRAIN=MAFF327195;  
 RA Suzuki F., Sawada H., Matsuda I.;  
 RT "Molecular Characterization of Toxoflavin Biosynthesis-related Gene in  
 Pseudomonas (Burkholderia) glumae";  
 RL Ann. Phytopathol. Soc. Jpn. 64:276-281(1998).

DR EMBL; AB040403; BAB88916.1; -;  
 DR GO; GO:0008703; F:5-amino-6-(5-phosphoribosylamino)uracil red. .; IEA.  
 DR GO; GO:0008835; F:diaminohydroxyphosphoribosylaminopyrimidine. .; IEA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0008270; F:zinc ion binding; IEA.  
 DR GO; GO:0009231; P:vitamin B2 biosynthesis; IEA.  
 DR InterPro; IPR002125; dCMP/cyt deam.

DR InterPro; IPR004794; Eubact ribD.  
 DR InterPro; IPR002734; RibD\_C.  
 DR Pfam; PF00383; dCMP\_cyt deam; 1.  
 DR Pfam; PF01872; RibD\_C; 1.  
 DR TIGRFAMs; TIGR00326; eubact ribD; 1.  
 DR PROSITE; PS00903; CYT dCMP DEAMINASES; 1.  
 SQ SEQUENCE 360 AA; 38449 MW; E4D8285B4D3A8D8 CRC64;

Query Match 35.3%; Score 49; DB 2; Length 360;  
 Best Local Similarity 47.8%; Pred. No. 29;  
 Matches 11; Conservative 1; Mismatches 7; Indels 4; Gaps 1;

QY 2 RPWTN-----CSLDGRSVLKTGT 20

RESULT 26

Query Match 34.9%; Score 48.5; DB 5; Length 1141;  
Best Local Similarity 48.1%; Pred. No. 1.3e+02;

```
Matches 13; Conservative 1; Mismatches 6; Indels 7; Gaps 1;
QY 6 NCSLDGRSVLK-----TGTTEKDVY 25
DB 742 NCLIDGRFVLKTSDFGLRLTTPSDFV 768

RESULT 28
Q8Y8W2 PRELIMINARY; PRT; 115 AA.
AC Q8Y8W2; 2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Hypothetical protein lmo0780.
GN LMO0780.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=EGD-e / Serovar 1/2a;
RA MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chatouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Feihl H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Gobel N., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kserst U., Kref J., Kuhn M., Kunst F., Kurapkak G.,
RA Madueno E., Moutounan A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordstiek G., Novellia S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL: AL591976; CAC98858.1; -.
DR PIR: A01172; A01172.
DR LDB: LMO0780; -.
DR Hypothetical protein; Complete proteome.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 115 AA; 13425 MW; 3D69674608FD8F9B CRC64;

Query Match 34.5%; Score 48; DB 16; Length 115;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 4 WTNCSLDGRSVLKT 17
DB 100 WAECCKQKAILKT 113

RESULT 29
Q8C4K3 PRELIMINARY; PRT; 250 AA.
AC Q8C4K3;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Tumor necrosis factor receptor superfamily.
GN TNFRSF18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Head;
RA MEDLINE=22354683; PubMed=12456851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
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DR EMBL: AK081878; BAC38357.1; -.
DR MGD: MGI:894675; Tnfrsf18.
DR GO: GO:0004872; P:receptor activity; IEA.
DR InterPro: IPR001368; TNFR_c6.
DR SMART: SM00208; TNFR; 2.
SQ SEQUENCE 250 AA; 27814 MW; 6963B94F414C16B4 CRC64;

Query Match 34.5%; Score 48; DB 11; Length 250;
Best Local Similarity 40.0%; Pred. No. 28;
Matches 10; Conservative 2; Mismatches 13; Indels 0; Gaps 0;
QY 1 CRPTWNCSLDGRSVLKTGTTEKDVY 25
DB 116 CRLWTNCSQFGFLTFPGNKTHNAV 140

RESULT 30
Q9N2W8 PRELIMINARY; PRT; 296 AA.
AC Q9N2W8;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN Y94H6A.7
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RA MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RC SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RA Wollam C., Zidanic M., Du H.;
RT "The sequence of C. elegans cosmid Y94H6A.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RC SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC024876; AAF60890.3; -.
DR HSSP: P24666; 5PNT.
DR WormPep: Y94H6A.7; CE29939.
DR GO: GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro: IPR00106; Low_mwt_PTPase.
DR Pfam: PF01451; LMWPC; 1.
DR PRINTS: PR00719; LMWTPASE.
DR SMART: SM00226; LMWPC; 1.
KW Hypothetical protein.
SQ SEQUENCE 296 AA; 33515 MW; CDA24424BEBE666 CRC64;

Query Match 34.5%; Score 48; DB 5; Length 296;
Best Local Similarity 60.0%; Pred. No. 34;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 4 WTNCSLDGRSVLKTG 18
DB 14 WTNFSLDGLLEIQKFG 28

RESULT 31
Q98SM6 PRELIMINARY; PRT; 651 AA.
ID Q98SM6
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Db      550 REPWTLAICENQNTLPSETSEQ 570
||||| : : : : : ||| : :
RESULT 33
Q8SYT9 PRELIMINARY; PRT; 415 AA.
ID AC
Q8SYT9
ID AC Q8SYT9
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RE34084p.
DE DE
GN CG8850.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
ON [1]_
RN RP
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RC RA
RC RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY071318; AAL48940.1; -.
RL FLYBase; FBgn0033708; CG8850.
DR DR GO; GO:0005887; C: integral to plasma membrane; IEA.
DR DR GO; GO:0016020; C: membrane; IEA.
DR DR GO; GO:0005328; F: neurotransmitter: sodium symporter activity; IEA.
DR DR GO; GO:0006836; F: neurotransmitter transport; IEA.
DR DR InterPro; IPR000175; Na/ntnra_symport.
DR DR Pfam; PF00209; SNF; 1.
DR DR PRINTS; PC00176; NANEUSMPORT.
DR DR ProDom; PD000448; Na/ntnra_symp; 1.
DR DR PROSITE; PS0267; NA_NEUROTRAN_SYMPT 3; 1.
DR DR SEQUENCE 415 AA; 45021 MW; 5433684459F62BF6 CRC64;
SQ
Query Match 34.2%; Score 47.5; DB 5; Length 415;
Best Local Similarity 47.4%; Pred. No. 59;
Matches 9; Conservative 4; Mismatches 5; Indels 1; Gaps
QY 3 PWTNCSLD-GRSVLKGTGT 20
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DB 160 PWTCLVEWGSQSVATGAT 178
ID AC
Q9V690 PRELIMINARY; PRT; 616 AA.
ID AC Q9V690
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG8850 protein.
DE DE
GN CG8850.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
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RN RP
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RC RC
RC RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Roques V.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
QY 3 PWTNCSLD-GRSVLKGTGT 20
||||| : : : : : ||| : :
DB 160 PWTCLVEWGSQSVATGAT 178
ID AC
Q9V690 PRELIMINARY; PRT; 616 AA.
ID AC Q9V690
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG8850 protein.
DE DE
GN CG8850.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
ON [1]_
RN RP
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
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RC RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Roques V.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA April J.F., Agabany A., An H.-J., Andrews-Pranngkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Borchman M.R., Bouck J., Brokstein P., Brothier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
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 RA Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Markulov G., Milshina N.V., Mccarty C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenhach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RA "The genome sequence of *Drosophila melanogaster*";  
 RA Science 287:2185-2195 (2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,  
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
 RA Bazan J., An H., Balgwin D., Banton J., Beeson K.Y., Busam D.A.,  
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
 RA Ferreira S., Frise E., Galle R.E., Garg N.S., George R.A.,  
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,  
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
 RA Stapleton M., Strong R., Svirkas R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 RA "Sequencing of *Drosophila melanogaster* genome";  
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,  
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,  
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 RA "Annotation of *Drosophila melanogaster* genome";  
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA FlyBase;  
 RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RN EMBL; AE003822; AAF58538.2; -  
 DR FlyBase; FBgn0033708; CG8850.  
 DR GO; GO:0005887; C:integral to plasma membrane; IEA.  
 DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005328; F:neurotransmitter:sodium symporter activity; IEA.  
 DR GO; GO:0006836; P:neurotransmitter transport; IEA.  
 DR InterPro; IPR000175; Na/intran\_symport.  
 DR Pfam; PF00209; SNF; 1.  
 DR PRINTS; PR00176; NANEUSMPORT.  
 DR ProDom; PD000448; Na/intran\_symport; 2.  
 DR PROSITE; PS00267; NA\_NEUROTRAN\_SYMPT\_3; 1.  
 SQ SEQUENCE 616 AA; 68093 MW; C9077B2DF8700A1F CRC64;  
 Query Match 34.2%; Score 47.5; DB 5; Length 616;  
 Best Local Similarity 47.4%; Pred. No. 91;  
 Matches 9; Conservative 4; Mismatches 5; Indels 1; Gaps 1;  
 QY 3 PWTNCSLD-GRSVLKTGTT 20  
 DB 160 PWTYCLVWKGKSCVATGAT 178  
 RESULT 35  
 ID P73915 PRELIMINARY; PRT; 119 AA.  
 AC P73915;  
 DT 01-FEB-1997 (TREMELrel. 02, Created)  
 DT 01-FEB-1997 (TREMELrel. 02, Last sequence update)  
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)  
 DE Transposase.  
 GN SLI1985.  
 OS Synchocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.  
 OX NCBI\_TaxID=1148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97061201; PubMed=8905231;  
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
 RA Miyajima N., Hikosawa M., Sugita M., Sasamoto S., Kimura T.,  
 RA Hosouchi T., Matsuura A., Muraki A., Nakazaki N., Naruo K., Okumura S.,  
 RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,  
 RA Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synchocystis sp. strain PCC6803. II. Sequence determination of the  
 RT entire genome and assignment of potential protein-coding regions.";  
 RL DNA Res. 3:1109-1136(1996).  
 DR EMBL; D90910; BAA17979.1; -  
 DR PIR; S75117; S75117.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005215; P:transporter activity; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR000515; BPD\_transp.  
 DR PROSITE; PS00402; BPD\_TRANSP\_INN\_MEMBER; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 119 AA; 14186 MW; F41C4622EBDDC246 CRC64;  
 Query Match 33.8%; Score 47; DB 16; Length 119;  
 Best Local Similarity 50.0%; Pred. No. 18;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 QY 2 RPWTNCSLDGRSVLKT 17  
 DB 104 RPWNQKVDGKTYLTT 119  
 RESULT 36  
 ID Q8BJV0 PRELIMINARY; PRT; 229 AA.  
 AC Q8BJV0;  
 DT 01-MAR-2003 (TREMELrel. 23, Created)  
 DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE Lymphotoxin-beta receptor precursor homolog (Fragment).  
 GN LTBR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
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RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).";
DR EMBL; AK078859; BAC37424.1; -.
DR MGD; MGI:104875; Ltbr.
FT NON TER
SQ SEQUENCE 229 AA; 24112 MW; 5A1C6870662B95F3 CRC64;

Query Match 33.8%; Score 47; DB 11; Length 229;
Best Local Similarity 32.0%; Pred. No. 37;
Matches 8; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 CRPWTNCSLDGRSVLKTGTTEKDV 25
Db 1 CQPHTRCEIQGLVEAPGTSYSDTI 25

RESULT 37
Q97EL8
ID Q97EL8 PRELIMINARY; PRT; 231 AA.
AC Q97EL8
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amidase, germination specific (cw1C/cw1D B.subtilis.
DE ortholog).
GN CAC3092.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VRM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omselchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.D., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AF007806; AAK81032.1; -.
DR PIR; E97280; E97280.
DR GO; GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.
DR GO; GO:0009253; P:peptidoglycan catabolism; IEA.
DR InterPro; IPR002508; Amidase_3.
DR Pfam; PF01520; Amidase_3; 1.
DR SMART; SM00646; Ami_3; 1.
KW Complete proteome.
SQ SEQUENCE 231 AA; 26138 MW; F9846AF0D4F93351 CRC64;

Query Match 33.8%; Score 47; DB 16; Length 231;
Best Local Similarity 56.2%; Pred. No. 37;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 9 LDGRSVLKTGTTEKDV 24
Db 50 IDGGANLKDGLTKDI 65

RESULT 38
Q8PIF1
ID Q8PIF1 PRELIMINARY; PRT; 306 AA.
AC Q8PIF1
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

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